

1/46

**FIGURE 1**

CGCCCGCGCGCGGGCTCAACTTTGTAGAGCGAGGGGCCAACTTGGCAGAGCGCGCGGCCA  
GCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGTGCGGGGACACGGGATCTACCCATACC  
ATTGACTAACTATGGAAGATTATACCAAAATAGAGAAAATTGGAGAAGGTACCTATGGAG  
TTGTGTATAAGGGTAGACACAAAACCTACAGGTCAAGTGGTAGCCATGAAAAAATCAGAC  
TAGAAAGTGAAGAGGAAGGGGTTCCCTAGTACTGCAATTCGGGAAATTTCTCTATTAAAGG  
AACTTCGTCATCCAAATATAGTCAGTCTTCAGGATGTGCTTATGCAGGATTCCAGGTTAT  
ATCTCATCTTTGAGTTTCTTTCCATGGATCTGAAGAAATACTTGGATTCTATCCCTCCTG  
GTCAGTACATGGATTCTTCACTTGTTAAGGTAGTAACACTCTGGTACAGATCTCCAGAAG  
TATTGCTGGGGTCAGCTCGTTACTCAACTCCAGTTGACATTTGGAGTATAGGCACCATAT  
TTGCTGAAGTAGCAACTAAGAAACCACTTTTCCATGGGGATTGAGAAATTGATCAACTCT  
TCAGGATTTTCAGAGCTTTGGGCACTCCCAATAATGAAGTGTGGCCAGAAGTGGAATCTT  
TACAGGACTATAAGAATACATTTCCCAATGGAAACCAGGAAGCCTAGCATCCCATGTCA  
AAAACTTGGATGAAAATGGCTTGGATTTGCTCTCGAAAATGTTAATCTATGATCCAGCCA  
AACGAATTTCTGGCAAAATGGCACTGAATCATCCATATTTTAATGATTTGGACAATCAGA  
TTAAGAAGATGTAGCTTTCTGACAAAAGTTTCCATATGTTATGTCAACAGATAGTTGTG  
TTTTTATTGTTAACTCTTGTCTATTTTTGTCTTATATATATTTCTTTGTTATCAAACCTC  
AGCTGTACTTCGTCTTCTAATTTCAAAAATATAACTTAAAAATGTAAATATTCTATATGA  
ATTTAAATATAATTCTGTAAATGTGAAAAAAAAAAAAAAAAAAAAA

2/46

**FIGURE 2**

MEDYTKIEKIGEGTYGVVYKGRHKTTGQVVAMKKIRLESEEEGVPSTAIRESLLKELRH  
PNIVSLQDVLMDLSRLYLIFEFLSMDLKKYLDSPPGQYMDSSLVKVVTWYRSPEVLLG  
SARYSTPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDY  
KNTFPKWKPGSLASHVKNLDENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDNQIKKM

cAMP- and cGMP-dependent protein kinase phosphorylation site.

217-220

Tyrosine kinase phosphorylation site.

9-15

N-myristoylation site.

27-32

43-48

134-139

164-169

190-195

Protein kinase domain

4-230

CCTCGGTTCTATCGATTGAATTGCCCGGGGATCCTCTAGAATGGAAAAGTACCACAGTGTT  
 GGAGATGATTGGAGAAGGCTCTTTTGGGAGGGTGTACAAGGGTGAAGAAAATACAGTGC  
 TCAGGTCGTGGCCCTGAAGTTCATCCCAAAATTGGGGCGCTCAGAGAAGGAGCTGAGGAA  
 TTTGCAACGAGAGATTGAAATAATCGGGGTCTGCGGCATCCCAACATTGTGCATATGCT  
 TGACAGCTTTGAACTGATAAAGAGGTGGTGGTGTGACAGACTATGCTGAGGAGAGCT  
 CTTTCAGATCCTAGAAGATGACGGAAAACCTCCTGAAGACAGGTTTTCAGGCCATTGCTGC  
 CCAGTTGGTGTGAGCCCTGTACTATCTGCATTCCCACCGCATCCTACACCGAGATATGAA  
 GCCTCAGAACATCCTCCTCGCCAAGGGTGGTGGCATCAAGCTCTGTGACTTTGGATTTCG  
 CCGGGCTATGAGCACCATAACAATTGGTGTGACATCCATCAAAGGCACACCACTTATAT  
 GTCTCCAGAGCTGGTGGAGGAGCGACCATACGACACACAGCGGACCTCTGGTCTGTTGG  
 CTGCATACATATAGACTGGCAGTAGGCACCCCTCCCTTCTATGCTACAAGCATCTTTTCA  
 GCTGGTCAGCCTCATTCTCAAGGACCCCTGTGCGCTGGCCCTCAACCATCAGTCCCTGCTT  
 TAAGAACTTCCTGCAGGGACTGCTCACCAGAGACCCACGGCAGCGACTGTCTGGCCAGA  
 CCTCTTATATCACCCCTTTATTTGCTGGTTCATGTACCATAATAACTGAGCCAGAGGCC  
 AGATTGTGGGACCCCATTCACAGCGCCCTACCCCCAGAAGCTTTCAGGTCCTAAGAGACA  
 ACAGGCCCATCGGTTGGCCCCCAAGGGTAATCAGTCTCGCATCTTGAAGTTCAGGCCTATAA  
 ACGCATGGCTGAGGAGGCCATGCAGAAGAAACATCAGAACACAGGACCTGCCCTTGAGCA  
 AGAGGACAAGACCAGCAAGGTGGCTCCTGGCACAGCCCTCTGCCAGACTCGGGGCCAC  
 TCCTCAGGAATCAAGCCTCCTGGCCGGGATCTTAGCCTCAGAATTGAAGAGCAGTGGGC  
 TAAATCAGGACTGGAGAGGTGCCCTCTGCACCTCGGAAAACCGGACCCAGCATTTG  
 TGAACGAGCATCTCCGAGGAGGAGGCCAGAGGTGCTGGGCCAGCGGAGCACTGATGTAGT  
 GGACCTGGAAAATGAGGAGCCAGACAGTGAACATGAGTGGCAGCACCTGCTAGAGACCAC  
 TGAGCCTGTGCCTATTCAACTGAAGGCTCCTCTCACCTTGCTGTGTAATCCTGACTTCTG  
 CCAGCGCATCCAGAGTCAGCTGCATGAAGCTGGAGGGCAGATCCTGAAGGCATCTTGA  
 GGGTGCTTCCCACATCTGCCCTGCATTCGGGTCTGAGCAGTCTTCTCTCAGCTGCAG  
 TGATTCTGTTGCTTGTATTCTTCTTGCCTGGGAGGAGCGGCTTCTGGGCTGCTGCTGAG  
 TCTACTCAGGCACAGTCAGGAGAGCAACAGCCTCCAGCAGCAATCTTGGTATGGGACCTT  
 CTTACAGGACCTGATGGCTGTGATTTCAGGCCTACTTTGCCTGTACCTTCAATCTGGAGAG  
 GAGCCAGACAAGTGACAGCCTCGAGGTGTTTTCAGGAGGCTGCCAACCTTTTCTGGACCT  
 GTTGGGGAACATGCTGGCCCAACAGATGACTCTGAGCAGACTTTGCGGAGGAGCAGCCT  
 TATGTGCTTTACTGTCTGTGCGAAGCCATGGATGGGAACAGCCGGGCCATCTCCAAAGC  
 CTTTTACTCCAGCTTGCTGACGACACAGCAGGTTGTCTTGGATGGGCTCCTTCATGGCTT  
 GACAGTTCCACAGCTCCCTGTCCACACTCCCCAAGGAGCCCCGCAAGTGAGCCAGCCACT  
 GCGAGAGCAGAGTGAGGATATACCTGGAGCCATTCTCTGCCCTGGCAGCCATATGCAC  
 TGCTCCTGTGGGACTGCCGACTGCTGGGATGCCAAGGACAGGCTGTGTTGGCATTTGGC  
 AAATCAGCTAACTGAAGACAGCAGCCAGCTCAGGCCATCCCTCATCTCTGGCCTGCAGCA  
 TCCCATCCTGTGCCTGCACCTTCTCAAGGTTCTATACTCCTGCTGCCTTGTGAGTGAGGG  
 CCTGTGCCGTCTTCTGGGGCAGGAGCCCTGGCCTTGAATCCCTGTTTATGTTGATTCA  
 GGGCAAGGTAAAAGTAGTAGATTGGGAAGAGTCTACTGAAGTGACACTTACTTCTCTC  
 CCTTCTTGTCTTTTCGGTCCAAAACCTAGCCTTGTGGAATTGGAGAAGCTAGGCAGTGAGCT  
 TGCTACTCTTTTACCCATTTCGCATGTGCTCTCTTGTGAGTGCAGCAGCCTGTCTATT  
 GGGACAGCTTGGTCAGCAAGGGGTGACCTTTGACCTCCAGCCCATGGAATGGATGGCTGC  
 AGCCACACATGCCTTGTCTGCCCTGCAGAGGTTGCGTTGACTCCACCAGGTAGTTGTG  
 ATTCTATGATGGCCTCCTTATCCTTCTGTTGACGCTCCTCACTGAGCAGGGGAAGGCTAG  
 CCTAATCAGGGATATGCTCAGTTTCAGAAATTGGACCGTTTGTGGCACCGCTGTCTCCAT  
 GGTCTGAGGCTCCCCGAGGAGGCATCTGCACAGGAAGGGGAGCTTTCGCTATCCAGTCC  
 ACCAAGCCCTGAGCCAGACTGGACACTGATTTCCTCCAGGGCATGGCAGCCCTGCTGAG  
 CCTGGCCATGGCCACCTTTACCCAGGAGCCCCAGTTATGCTGAGCTGCCTGTCCCAGCA  
 TGGAAGTATGCTCATGCTCCATCTGAAGCATCTGCTTGTGCCAGCTTCTTGAATCAACT  
 CGCCAGGCGCCTCATGGCTCTGAGTTTCTGCTTCTGCTGCTGCTCTGTCTGCCAGCT  
 CCTTTGCTTCCCTTTGCGCTGGACATGGATGCTGACCTCCTTATAGTTGTCTTGGCCGA  
 CCTCAGGACTCAGAAGTTGCAGCCCATCTGCTGCAGGTCTGCTGCTACCATCTTCCGTT  
 GATGCAAGTGGAGCTGCCCATCAGCCTTCTCACAGCCTGGCCCTCATGGATCCCACCTC  
 TCTCAACAGCTTTGTGAACACAGTGTCTGCCCTCCCCTAGAACCATCGTCTGTTTCTC  
 AGTTGCCCTCTGAGTGACCAAGCACTGTTGACCTCCGACCTTCTCTCTGCTGGCCCA  
 TACTGCCAGGGTCTGTCTCCCAGCCACTTGTCTTTATCCAAGAGCTTCTGGCTGGCTC  
 TGATGAATCCTATCGGCCCTGCGCAGCCTCCTGGGCCACCCAGAGAATTCTGTGCGGGC  
 ACACACTTATAGGCTCCTGGGACACTTGTCTCAACACAGCATGGCCCTGCTGGGGCACT  
 GCAGAGCCAGTCTGGACTGCTCAGCCTTCTGCTGCTTGGGCTGGAGACAAGGATCCTGT  
 TGTGCGGCTGCAGTGCCAGCTTGTCTGTGGCAATGCAGCCTACCAGCTGGTCTCTGGG  
 ACCTGCCCTGGCAGCTGCAGTGCCAGTATGACCCAGCTGCTTGGAGATCCTCAGGCTGG  
 TATCCGGCGCAATGTTGCATCAGCTCTGGGCAACTTGGGACCTGAAGGTTTGGGAGAGGA

4/46

**FIGURE 3B**

GCTGTTACAGTGCGAAGTACCCCAGCGGCTCCTAGAAATGGCATGTGGAGACCCCAGCC  
AAATGTGAAGGAGGCTGCCCTCATTGCCCTCCGGAGCCTGCAACAGGAGCCTGGCATCCA  
TCAGGTACTGGTGTCCCTGGGTGCCAGTGAGAACTATCCTTGCTCTCTCTGGGGAATCA  
GTCAGTGCACACAGCAGTCCTAGGCCTGCCTCTGCCAAACACTGCAGGAAACTCATTCA  
CCTCCTGAGGCCAGCCATAGCATGTGAAGCTTGGCCGCCATGGCCC

5/46

**FIGURE 4A**

MEKYHVLEMIGEGSFGRVYKGRRKYSAQVVALKFIPKLGRSEKELRNLOREIEIMRGLRH  
 PNIVHMLDSFETDKEVVVVVTDYAEGELFQILEDDGKLPEDQVQAIQAQLVSALYYLHSHR  
 ILHRDMKPKQNILLAKGGGIKLCDFGFARAMSTNTMVLTSIKGTPLYMSPELVEERPYDHT  
 ADLWSVGCILYELAVGTPPFYATSIFQLVSLILKDPVRWPSTISPCFKNFLQGLLTKDPR  
 QRLSWPDLLYHPFIAGHVTTIITEPAGPDLGTPFTSRLPPELQVLKDEQAHRLAPKGNQSR  
 ILTQAYKRMAEEAMQKKHQNTGPALQEDKTSKVAPGTAPLPRLGATPQESSLLAGILAS  
 ELKSSWAKSGTGEPVPSAPRENRTTPDCERAFPEERPEVLGQRSTDVVDLENEEPDSDNEW  
 QHLETTEPVPIQLKAPLTLLCNPDFCQRIQSOLHEAGGQILKGILEGASHILPAFRVLS  
 SLLSSCSDSVALYSFCREAGLPGLLLSLLRHSQESNSLQQQSWYGTFLQDLMAVIQAYFA  
 CTFNLERSQTSDSLQVFOEAAANFLDLLGKLLAQPDSEQTLRRDSLMTCTVLCEAMDGN  
 SRAISKAFYSSLLTTQQVVLGILLHGLTVPQLPVHTPQGAPQVSQPLREQSEDIPGAISS  
 ALAAICTAPVGLPDCWDAKEQVCWHLANQLTEDSSQLRPSLISGLQHPILCLHLLKVLVS  
 CCLVSEGLCRLLGQEPPLALESFLMLIQGKVKVVDWEESTEVTLTYFLSLLVFRLLQNLPCGM  
 EKLGSVDVATLFTSHSVVSLVSAAACLLGQLGQQGVTFDLQPMEWMAAATHALSAPAEVRL  
 TPPGSCGFYDGLLILLQLLQTEQGKASLIRDMSSSEMWTVLWHRFSMVLRLPEEASAEQEG  
 ELSLSSPPSPPEPDWTLISPOGMAALLSLAMATFTQEPQLCLSCLSQHGSILMSILKHLIC  
 PSFLNQLRQAPHGSEFLPVVVLVSVQQLCFPFALDMDADLLIVVLADLRDSEVAHLLQV  
 CCYHLPLMQVELPISLLTRLALMDPTSLNQFVNTVSASPTIVSFLSVALLSDQPLLTSD  
 LLSLLAHTARVLSPSHLSFIQELLAGSDESYRPLRSLLGHPENSVRAHTYRLLGHLLOHS  
 MALRGALQSQSGLLSLLLLGLGDKDPVVRCSASFVGNAAAYQAGPLGPALAAAVPSMTQL  
 LGDPQAGIRRNVASALGNLGPGLGEELLQCEVPQRLLMACGDPQPNVKEAALIALRSL  
 QQEPGIHQVLVSLGASEKLSLLSLGNQSLPHSSPRPASAKHCRKLIHLLRPAHSM

N-glycosylation site.

297-300  
 381-384  
 1286-1289

Glycosaminoglycan attachment site.

369-372

cAMP- and cGMP-dependent protein kinase phosphorylation site.

23-26  
 583-586

N-myristoylation site.

138-143  
 270-275  
 356-361  
 400-405  
 464-469  
 503-508  
 599-604  
 622-627  
 656-661  
 671-676  
 784-789  
 1106-1111  
 1145-1150  
 1207-1212

Amidation site.

20-23

6/46

**FIGURE 4B**

Leucine zipper pattern.

769-790  
987-1008

Serine/Threonine protein kinases active-site signature.

121-133

Protein kinase domain  
1-294

7/46

**FIGURE 5A**

CAGAGCAGGGCGAGAGCCGATCAGCGGATCACCGAGTCTCGCCAGGTGGTGGAGCTGGCA  
GTGAAGGAGCACAAGGCTGAGATTCTCGCTCTGCAGCAGGCTCTCAAAGAGCAGAAGCTG  
AAGGCCGAGAGCCTCTCTGACAAGCTCAATGACCTGGAGAAGAAGCATGCTATGCTTGA  
ATGAATGCCCCAAGCTTACAGCAGAAGCTGGAGACTGAACGAGAGCTCAAACAGAGGCTT  
CTGGAAGAGCAAGCCAAATTACAGCAGCAGATGGACCTGCAGAAAAATCACATTTTCCGT  
CTGACTCAAGGACTGCAAGAAGCTCTAGATCGGGCTGATCTACTGAAGACAGAAAGAAGT  
GACTTGGAGTATCAGCTGGAAAACATTACAGGTTCTCTATTCTCATGAAAAGGTGAAAATG  
GAAGGCACTATTTCTCAACAAACCAAACCTCATTGATTTTCTGCAAGCCAAAATGGACCAA  
CCTGCTAAAAAGAAAAAGGTTCTCTGCAGTACAATGAGCTGAAGCTGGCCCTGGAGAAG  
GAGAAAAGCTCGCTGTGCAGAGCTAGAGGAAGCCCTTCAGAAGACCCGCATCGAGCTCCGG  
TCCGCCCGGGAGGAAGCTGCCACCGCAAAGCAACGGACCACCCACACCCATCCACGCCA  
GCCACCGCGAGGCAGCAGATCGCCATGTCTGCCATCGTGCGGTGCGCCAGAGCACCAGCCC  
AGTGCCATGAGCCTGTGGCCCCGCCATCCAGCCGCAGAAAGGAGTCTTCAACTCCAGAG  
GAATTTAGTCGGCGTCTTAAGGAACGCATGCACCACAATATTCTCACCAGATTCAACGTA  
GGACTGAACATGCGAGCCCAAAGTGTGCTGTGTCTGGATAACCGTGCACTTTGGACGC  
CAGGCATCCAAATGTCTCGAATGTGAGGTGATGTGTGTCACCCCAAGTGCTCCACGTGCTTG  
CCAGCCACCTGCGGCTTGCTGTGAATATGCCACACACTTCACCGAGGCTTCTGCCGT  
GACAAATGAAGTCCCCAGGTCTCCAGACCAAGGAGCCAGCAGCAGCTTGACCTGGAA  
GGGTGGATGAAGGTGCCAGGAATAACAAACGAGGACAGCAAGGCTGGGACAGGAAGTAC  
ATTGTCTGGAGGGATCAAAGTCTCATTTATGACAATGAAGCCAGAGAAGCTGGACAG  
AGGCCGCTGGAAGAATTTGAGCTGTGCCCTCCCGACGGGGATGTATCTATTATGTTGCC  
GTTGGTGCTTCCGAAGTCCGAAATACAGCCAAAGCAGATGTCCATACATACTGAAGATG  
GAATCTCACCCGCACACCACCTGCTGGCCCCGGGAGAACCCTCTACTTGTAGCTCCAGC  
TTCCCTGACAAACAGCGCTGGGTACCCGCTTAGAATCAGTTGTGCGAGGTGGGAGAGTT  
TCTAGGAAAAAGCAGAAGCTGATGCTAAAGTCTTGGAAACTCCCTGCTGAAACTGGAA  
GGTGATGACCGTCTAGACATGAAGTGCACGCTGCCCTTCAGTGACCAGGTGGTGTGGTG  
GGCACCAGGAAGGGCTCTACGCCCTGAATGTCTTGAAAACTCCCTAACCCTATGTCCCA  
GGAATTTGAGCAGTCTTCCAAATTTATATTTATCAAGGACCTGGAGAAGCTACTCATGATA  
GCAGGAGAAGAGCGGGCACTGTGTCTTGTGGACGTGAAGAAAGTGAACAGTCCCTGGCC  
CAGTCCACCTGCTGCCCCAGCCCCGACATCTACCCCAACATTTTGAAGCTGTCAAGGGC  
TGCCACTTGTTTGGGGCAGGCAAGATTGAGAACGGGCTCTGCATCTGTGCAGCCATGCCC  
AGCAAAGTCGTCTATTCTCCGCTACAACGAAAACCTCAGCAAATACTGCATCCGGAAGAG  
ATAGAGACCTCAGAGCCCTGCAGCTGTATCCACTTCACCAATTACAGTATCCTCATTTGA  
ACCAATAAATTTACGAAATCGACATGAAGCAGTACACGCTCGAGGAATTCCTGGATAAG  
AATGACCATTTCTTGGCACCTGCTGTGTTTGGCGCTTTCACACAGCTTCCCTGTCTCA  
ATCGTGCAGGTGAACAGCGCAGGGCAGCGAGAGGAGTACTTGCTGTGTTTCCACGAATTT  
GGAGTGTTCGTGGATTCTTACGGAAGACGTAGCCGCACAGACGATCTCAAGTGGAGTCGC  
TTACCTTTGGCCTTTGCTTACAGAGAACCCCTATCTGTTTGTGACCCACTTCAACTCACTC  
GAAGTAATTGAGATCCAGGCACGCTCCTCAGCAGGGACCCCTGCCGAGCGTACCTGGAC  
ATCCCGAACCCGCGCTACCTGGGCCCTGCCATTTCTCAGGAGCGATTACTTGGCGTCC  
TCATACCAGGATAAATTAAGGGTCATTTGCTGCAAGGGAAACCTCGTGAAGGAGTCCGGC  
ACTGAACACCACCGGGGCCCCGTCCACCTCCCGCAGCAGCCCCAACAAAGCGAGGCCACCC  
ACGTACAACGAGCAGATCACCAAGCGCGTGGCCTCCAGCCAGCGCCGCCCCGAAGGCCCC  
AGCCACCCGCGAGGCAAGCACACCCACCGCTACCGCGAGGGGCGGACCCGAGCTGCGC  
AGGGACAAGTCTCCTGGCCGCCCTTGGAGCGAGAGAAGTCCCCCGCCGGATGCTCAGC  
ACGCGGAGAGAGCGGTCCCCGGGAGGCTGTTTGAAGACAGCAGCAGGGGCGCGGTGCCT  
GCGGGAGCCGTGAGGACCCCGCTGTCCAGGTGAACAAGTCTGGGACCAAGTCTTCAGTA  
TAAATCTCAGCCAGAAAAACCAACTCCTCATCTTGATCTGCAGGAAAAACCAAACACAC  
TATGGAACCTGCTGATGGGGACCCAAGCGCCACGTGCTCAGCCACCCCTCTGGCTCAGC  
GGGGCCCAAGCAACCTCGGCACGGACACCCCTGTCTCAGGAGGGGCGAGGTGGCTGAGG  
CTCTTCGGAGCTGTGACGCCCCGGTGCCCTGCCCTGGGCACCTCCCTGCAGTCATCTCTTT  
GCACTTTGTTACTCTTTCAAAGCATTACAAACTTTTGTACCTAGCTCTAGCCTGTACCA  
GTTAGTTTCATCAAAGGAACCAACCGGGATGCTAACAAACATGGTTAGAATCCTAATT  
AGCTACTTTAAGATCCTAGGATTGGTTGGTTTTTCTTTTTTTTTTCTTTTGTCTTTT  
CTTTTTTTTTTTTTTTTAAAGACAACAGAATTCCTTAATAGATTGAATAGCGACGTATT  
TCCTGTTGTAGTCATTTTTAGCTCGACCACATCATCAGGTCTTTGCCACCGAGGCATAGT  
GTAGAACAGTCCCGGTCAAGTTGGCCAACCTCCCGCAGCCAAGTAGGTTTCATCCTTGTTC  
TGTTTCATTCTCATAGATGGCCCTGCTTTCCCCAGGGTGACATCGTAGCCAAATGTTTACT  
GTTTTTCATTGCTTTTATGGCCTTGACGACTTCCCTCCACAGCTGAGAATGTATGGA  
GTTTCATCGGGGCTCAGCTCGGAGGCGAGTACTTGGGGCCAAGGGACCTCGAGACGCTTT  
CCTTCCCCACCCCCCAGCGTCATCTCCCCAGCCTGCTGTTCCCGCTTTCCATATAGCTTT  
GGCCAGGAAGCATGCAATAGACTTGCTCGGAGCCAGCACTCCTGGGTCTCGGGGTGCG

8/46

**FIGURE 5B**

GGAGGGGACGGGGGCACCCACTTCCTTGCTGTGACGGCGTGTTGTTCCCCACTCTGGGA  
TGGGGAAGAGGCCCCGTCGGGAGTTCTGTCATGGCAGTTCAGTGCATGTGCTGCCCCCTTGG  
GTTGCTCTGCCAATGTATTAATACCATCCCATAGCTCCTGCCAAATCGAGACCCCTCTGAC  
GACTTGCCGACTAACTGGCCACCACAAGCTGCAGTCTGTAGCACTGAACAAACAAAAAAC  
AAAACGCTCAAGCCTTACGACCAGAGAAGGATTTTCAGCAAACCACCACCTCCCACTCAGT  
GTCCCCCTCCAAACTTCACACTTCCCTGCCTGCAGAGGATGACTCTGTTTACACCCAATCC  
AGCGCGGTTCTACCCACGAACTGTGACTTTCCAAATGAGCCTTTCCCTAGGGCTAGAC  
CTAAGACCAGGAAGTTTGAGAAAGCAGCCGAGCTCAACTCTTCCAGCTCCGCCAGGGTT  
GGGAAGTCCTTAGGTGCAGTGGGGCTCCCACTGGGTCTGCGGACCCTCCTATTAGAGTAC  
GAAATTCCTGGCAACTGGTATAGAACCAACCTAGAGGCTTTGCAGTTGGCAAGCTAACTC  
GCGGCCTTATTTCTGCCTTTAATCTCCACAAGGCATCTGTTGCTTTGGGTCTCCACGA  
CTCTTAGGCCCCGCTCAACAACCCAGGCACCTCCTAGGTAGGCTCAAAGGTAGACCCGTT  
TCCACCGCAGCAGGTGAACATGACCGTGTTTTCAACTGTGTCCACAGTTCAGATCCCTTT  
CCAGATTGCAACCTGGCCTGCATCCCAGCTCCTTCTGCTCGTGTCTTAACCTAAGTGCT  
TTCTTGTTTGAAACGCCTACAAACCTCCATGTGGTAGCTCCTTTGGCAAATGTCTGCTG  
TGGCGTTTTATGTGTTGCTTGGAGTCTGTGGGGTCGTACTCCCTCCCGTCCCCAG  
GGCAGATTTGATTGAATGTTTGCTGAAGTTTTGTCTCTTGGTCCACAGTATTTGGAAAGG  
TCACTGAAAATGGGTCTTTCAGTCTTGGCATTTCATTTAGGATCTCCATGAGAAATGGGC  
TTCTTGAGCCCTGAAAATGTATATTGTGTGTCTCATCTGTGAAGTCTTTCTGCTATATA  
GAACTAGCTCAAAAGACTGTACATATTTACAAGAACTTTATATTCGTAAAAAAGGAG  
AGGAAATTGAATTGGTTTCTACTTTTTTATTGTAAAAGGTGCATTTTTCAACACTTACTT  
TTGGTTTCAATGGTGGTAGTTGTGGACAGCCATCTTCACTGGAGGGTGGGGAGCTCCGTG  
TGACCACCAAGATGCCAGCAGGATATACCGTAACACGAAATTGCTGTCAAAGCTTATTA  
GCATCAATCAAGATTCTAGGTCTCCAAAAGTACAGGCTTTTCTTCACTTACCTTTTTTAT  
TCAGAACGAGGAAGAGAACACAAGGAATGATTCAAGATCCACCTTGAGAGGAATGAACCTT  
TGTTGTTGAACAATTAGTGAAATAAAGCAATGATCTAAACT



9/46

**FIGURE 6**

MLEMNARSLQOKLETERELKQRLLEEQAQLQQQMDLQKNHIFRLTQGLQEALDRADLLKT  
 ERSLEYQLENIQVLYSHEKVKMEGTISQOTKLIDFLQAKMDQPAKKKKVPLQYNELKLA  
 LEKEKARCAELEELQKTRIELRSAREEAHRKATDHPHPSTPATARQQIAMSIVRSPE  
 HQPSAMSLAPPSSRRKESSTPEEFSRRLKERMHHNIPHRFNVGLNMRATKCAVCLDTVH  
 FGRQASKCLECQVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSL  
 HLEGWMKVPRNNKRGQQGWDKRYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSI  
 HGAVGASELANTAKADVPIILKMESHPTTCWPGRTLYLLAPSFDPKQRWVTALESVVAG  
 GRVSREKAEADAKLLGNSLLKLEGDDRLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLT  
 HVPGIGAVFQIYI IKDLEKLLMIAGEERALCLVDVKVKQSLAQSHLPAQPDISPNI FEA  
 VKGCHLFGAGKIENGLCICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSI  
 LIGTNKFYEIDMKQYTLEEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCF  
 HEFGVFVDSYGRRSRTDDLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARA  
 YLDIPNPRYLGPATSSGAIYLAASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKR  
 GPPTYNEHITKRVASSPAPPEGPSHPREPSTPHRYREGRTELRRDKSPGRPLEREKSPGR  
 MLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNVWDQSSV

N-glycosylation site.

451-454  
 574-577  
 597-600

cAMP- and cGMP-dependent protein kinase phosphorylation site.

152-155  
 196-199

N-myristoylation site.

47-52  
 362-367  
 420-425  
 464-469  
 555-560

Amidation site.

670-673

Carbamoyl-phosphate synthase subdomain signature 2.

1-8

CNH domain  
 448-745

PH domain  
 300-419

Phorbol esters/diacylglycerol binding domain  
 219-267

10/46

**FIGURE 7**

AAAGGCCTGCAGCAGGACGAGGACCTGAGCCAGGAATGCAGGATGGCGGCGGTGAAGAAAG  
GAAGGGGGTGCTCTGAGTGAAGCCATGTCCCTGGAGGGAGATGAATGGGAACTGAGTAAA  
GAAAATGTACAACCTTTAAGGCAAGGGCGGATCATGTCCACGCTTCAGGGAGCACTGGCA  
CAAGAATCTGCCTGTAACAATACTCTTCAGCAGCAGAAACGGGCATTTGAATATGAAATT  
CGATTTTACACTGGAATGACCTCTGGATGTTTGGGATAGGTATATCAGCTGGACAGAG  
CAGAACATCCTCAAGGTGGGAAAGAGAGTAATATGTCAACGTTATTAGAAAAGAGCTGTA  
GAAGCACTACAAGGAGAAAACGATATTATAGTGATCCTCGATTTCTCAATCTCTGGCTT  
AAATTAGGGCGTTTATGCAATGAGCCTTTGGATATGTACAGTTACTTGCACAACCAAGGG  
ATTGGTGTTTCTCAGTTCTATATCTCATGGGCGAGAAGAAATATGAAGCTAGAGAA  
AATTTAGGAAAGCAGATGCGATATTTAGGAAGGGATTCAACAGAAGGCTGAACCACTA  
GAAAGACTACAGTCCCAGCACCGACAATTCCAAGCTCGAGTGCTCTCGGCAAACTCTGTTG  
GCACTTGAGAAAGAAGAAGAGGAGGAAGTTTGTGAGTCTTCTGTACCACAACGAAGCACA  
CTAGCTGAACATAAGAGCAAAGGGAAAAAGACAGCAAGAGCTCCAATCATCCGTGTAGGA  
GGTGCTCTCAAGGCTCCAAGCCAGAACAGAGGACTCCAAAATCCATTTCCCTCAACAGATG  
CAAAATAATAGTAGAATTACTGTTTTTGTATGAAAATGCTGATGAGGCTTCTACAGCAGAG  
TTGTCTAAGCCTACAGTCCAGCCATGGATAGCACCCCCCATGCCCCAGGGCCAAAGAGAAT  
GAGCTGCAAGCAGGCCCTTGGAACACAGGCAGGTCTTGGAACACAGGCCTCGTGGCAAT  
ACAGCTTCACTGATAGCTGTACCGCTGTGCTTCCAGTTTCACTCCATATGTGGAAGAG  
ACTGCACAACAGCCAGTTATGACACCATGTAAAATTGAACCTAGTATAAACCCACATCCTA  
AGCACCAGAAAGCCTGGAAAGGAAGAGGAGATCCTCTACAAAGGGTTCAGAGCCATCAG  
CAAGCGTCTGAGGAGAAGAAAGAGAAGATGATGTATTGTAAGGAGAAGATTTATGCAGGA  
GTAGGGGAATTTCTCCTTTGAAGAAATTCGGGCTGAAGTTTCCGGAAGAAATTTAAAGAG  
CAAAGGGAGCCGAGCTATTGACCAGTGACAGAGAAGAGAGCAGAAATGCAGAAACAGATT  
GAAGAGATGGAGAAGAAGCTAAAAGAAATCCAACTACTCAGCAAGAAAGAACAGGTGAT  
CAGCAAGAAGAGACGATGCTTACAAAGGAGACAACATAAAGTCAAATTTGCTTCCGAGTCT  
CAGAAAATACCAGGAATGACTCTATCCAGTTCTGTTTGTCAAGTAACTGTTGTGCCAGA  
GAACTTCACTTGCGGAGAACATTTGGCAGGAACAACCTCATTTAAAGGTCCAGTGTA  
CCTTTCTCCATTTTGTATGAGTTTCTTCTTTTCAAGAAAGAAGAAATAAAGTCTCTGCA  
GATCCCCACGAGTTTGTCTCAACGAAGACCCCTTGAGTTCTCAAACCTCAGAAAGC  
ATCACCTCAAATGAAGATGTGTCTCCAGATGTTTGTGATGAATTTACAGGAATTGAACCC  
TTGAGCGAGGATGCCATTATCACAGGCTTCAGAAATGTAACAATTTGTCTTAACCCAGAA  
GACACTTGTGACTTTGCCAGAGCAGCTCGTTTTGTATCCACTCCTTTTCATGAGATAATG  
TCCTTGAAGGATCTCCCTTCTGATCCTGAGAGACTGTTACCGGAAGAAGATCTAGATGTA  
AAGACCTCTGAGGACAGCAGACTTGTGGCACTATCTACAGTCAGACTCTCAGCATC  
AAGAAGCTGAGCCCAATTATTGAAGACAGTCGTGAAGCCACACACTCCTCTGGCTTCTCT  
GGTCTTCTGCCTCGGTTGCAAGCACCTCCTCCATCAAATGTCTTCAAATTCCTGAGAAA  
CTAGAACTTACTAATGAGACTTCAGAAAACCTACTCAGTCACCATGGTGTTCACAGTAT  
CGCAGACAGCTACTGAAGTCCCTACCAGAGTTAAGTGCTCTGCAGAGTTGTGTATAGAA  
GACAGACCAATGCTTAAGTTGGAATTTGAGAAGGAAATTTGAATAGGTAATGAGGATTAC  
TGCATTAAACGAGAATACCTAATATGTGAAGATTACAAGTTATTCTGGGTGGCGCCAAGA  
AACTCTGCAGAATTAACAGTAATAAAGGTATCTTCTCAACCTGTCCCATGGGACTTTTAT  
ATCAACCTCAAGTTAAAGGAACGTTTAAATGAAGATTTTGTATCATTTTTTGCAGCTGTTAT  
CAATATCAAGATGGCTGTATTGTTTGGCACCAATATATAAAGTCTTCAACCTTCAGGAT  
CTTCTCCAACACAGTGAATATATTACCCATGAAATAACAGTGTTGATTATTTATAACCTT  
TTGACAATAGTGGAGATGCTACACAAAGCAGAAATAGTCCATGGTGACTTGAGTCCAAGG  
TGTCTGATTCTCAGAAACAGAATCCACGATCCCTATGATTGTAACAAGAACAATCAAGCT  
TTGAAGATAGTGGACTTTTCTACAGTGTTGACCTTAGGGTGCAGCTGGATGTTTTTACC  
CTCAGCGGCTTTTCGAGCTGTACAGATCCTGGAAGGACAAAAGATCCTGGCTAACTGTTCT  
TCTCCCTACCAGGTAGACCTGTTTGGTATAGCAGATTTAGCACATTTACTATTGTTCAAG  
GAACACCTACAGGTCTTCTGGGATGGGTCTTCTGGAACCTTAGCCAAAATATTTCTGAG  
CTAAAAGATGGTGAATTGTGGAATAAATCTTTGTGCGGATTCTGAATGCCAATGATGAG  
GCCACAGTGTCTGTTCTTGGGGAGCTTGACGAGCAAAATGAATGGGGTTTTTGCAGCTACA  
TTCCAAAGTCACCTGAACAAAGCCTTATGGAAGGTAGGGAAGTTAACTAGTCTGGGGCT  
TTGCTCTTTTCAAGTGAAGTCAAGTCTCACAGATTGCTGCCTCAGAGCAATGGTT  
GTATTGTGGAACACTGAACTGTATGTGCTGTAATTTAATTTAGGACACATTTAGATGCA  
CTACCATTGCTGTTCTACTTTTTTGGTACAGGTATATTTTGCAGTCACTGATATTTTTTAT  
ACAGTGATATACTTACTCATGGCCTTGTCTAACTTTTTGTGAAGAACTATTTTATTCTAAA  
CAGACTCATTACCAATGGTTACCTTGTATTATTAACCCATTTGTCTCTACTTTTCCCTGTA  
CTTTTCCCAATTTGTAATTTGTAAATGTTCTCTTATGATCACCATGATTTTGTAAATAA  
TAAATAGTATCTGTTAAAAA

11/46

**FIGURE 8**

MAAVKKEGGALSEAMSLEGDEWELSKENVQPLRQGRIMSTLQGALAQESACNNTLQQQKR  
 AFEYEIRFYTGNDPLDVWDRIYISWTEQNYPQGGKESNMSTLLERAVEALQGEKRYISDPR  
 FLNLWLKLGRLCNEPLDMYSYLNQGGIGVSLAQFYISWAEYEARENFRKADAIHQEGIQ  
 QKAEPLERLQSQHRQFQARVSRQTLLEKEEEEEVFESSVPQRSTLAEKSKGKKTARA  
 PIIRVGGALKAPSONRGLQNPFFQOMQNNRITVFDENADEASTAELSKPTVQPWIAPPM  
 PRAKENELQAGPWNTGRSLEHRPRGNTASLIAPVAVLPSFTPYVEETAQQPVMTCKIEP  
 SINHILSTRKPGKEEGDPLQRVQSHQQASEEKKEKMMYCKEKIYAGVGEFSFEEIRAEVF  
 RKKLKEQREAEELLTSAEKRAEMQKQIEEMKKLKEIQTTQQERTGDQQEETMPTKETTKL  
 QIASSEKQIPGMTLSSSVCQVNCCARETSLAENIWQEQPHSKGPSVPFSIFDEFLLEKK  
 NKSPPADPPRVLAQRRPLAVLKTSESITSNEDVSPDVCDEFTGIEPLSEDAIITGFRNVT  
 ICPNPEDTCDFAARAARFVSTPFHEIMSLKDLPSDPERLLPEEDLDVKTSEDQQTACGTIY  
 SQTLSIKKLSPIIEDSREATHSSGFGSSASVASTSSIKCLQIPEKLELTNETSENPTQS  
 PWCSQYRRQLLKSLPELSASAELCIEDRPMPEKLEIEKEIELGNEDYCIKREYLICEDYKL  
 FWVAPRNSAELTVIKVSSQPVWDFYINLKLKERLNEDFDHFCSCYQYQDGCIVWHQYIN  
 CFTLQDLLQHSEYITHEITVLIINYLLTIVEMLHKAIEIVHGDLSRCLILRNRIHDPYDC  
 NKNNQALKIVDFSYSDLRVQLDVFTLSGFRTVQILEGQKILANCSSPYQVDLFGIADLA  
 HLLLKFKEHLQVFDGSEFWKLSQNISELKDGELWNKFFVRILNANDEATVSVLGELAAEMN  
 GVFDTTTFQSHLNKALWKVGKLTSPGALLFQ

N-glycosylation site.

52-55  
 97-100  
 268-271  
 598-601  
 711-714  
 944-947  
 983-986

cAMP- and cGMP-dependent protein kinase phosphorylation site.

667-670

Tyrosine kinase phosphorylation site.

908-914

N-myristoylation site.

8-13  
 92-97  
 146-151  
 148-153  
 325-330  
 491-496  
 657-662  
 687-692  
 1021-1026

Amidation site.

233-236

12/46

**FIGURE 9**

GGAAGACTTGGGTCTTGGGTGCGCAGGTGGGAGCCGACGGGTGGGTAGACCGTGGGGGAT  
ATCTCAGTGGCGGACGAGGACGGCGGGGACAAGGGGCGGCTGGTCCGAGTGGCGGAGCGT  
CAAGTCCCCTGTGCGTTCCCTCCGTCCCTGAGTGTCTTGGCGCTGCCTTGTGCCCGCCCA  
GCGCCTTTGCATCCGCTCCTGGGCACCGAGGCGCCCTGTAGGATACTGCTTGTACTTAT  
TACAGCTAGAGGCATCATGGACCGATCTAAAGAAAACCTGCATTTAGGACCTGTTAAGGC  
TACAGCTCCAGTTGGAGGTCCAAAACGTGTTCTCGTGACTCAGCAAATTCCTTGTGAGAA  
TCCATTACCTGTAAATAGTGGCCAGGCTCAGCGGGTCTTGTGTCTTCAAATTCCTCCCA  
GCGCGTTCCCTTTGCAAGCACAAAAGCTTGTCTCCAGTCACAAGCCGGTTTCAAGATCAGAA  
GCAGAAGCAATTGCAGGCAACCAAGTGTACCTCATCTGTCTCCAGGCCACTGAATAACAC  
CCAAAAGAGCAAGCAGCCCCCTGCCATCGGCACCTGAAAATAATCCTGAGGAGGAACCTGGC  
ATCAAAACAGAAAAATGAAGAATCAAAAAAGAGGCAGTGGGCTTTGGAAGACTTTGAAAT  
TGGTCGCCCTCTGGGTAAAGGAAAGTTTGGTAATGTTTATTTGGCAAGAGAAAAGCAAAG  
CAAGTTTATTCTGGCTCTTAAAGTGTTATTTAAAGCTCAGCTGGAGAAAAGCCGGAGTGGA  
GCATCAGCTCAGAAGAGAAGTAGAAATACAGTCCACCTTCGGCATCCTAATATTCTTAG  
ACTGTATGGTTATTTCCATGATGCTACCAGAGTCTACCTAATTCCTGGAATATGCACCACT  
TGGAACAGTTTATAGAGAACCTTCAGAACTTTCAAAGTTTGATGAGCAGAGAAGTGTCTAC  
TTATATAACAGAATTGGCAAATGCCCTGTCTTACTGTCTATTGCAAGAGAGTTATTCATAG  
AGACATTAAGCCAGAGAACCTTACTTCTTGGATCAGCTGGAGAGCTTAAAATTGCAGATTT  
TGGGTGGTCAGTACATGCTCCATCTTCCAGGAGGACCACTCTCTGTGGCACCCTGGACTA  
CCTGCCCCCTGAAATGATTGAAGGTCGGATGCATGATGAGAAGGTGGATCTCTGGAGCCT  
TGGAGTTCTTTGCTATGAATTTTTAGTTGGGAAGCCTCCTTTTGAGGCAAACACATACCA  
AGAGACCTACAAAAGAATATCACGGGTGAATTCACATTCCTGACTTTGTAACAGAGGG  
AGCCAGGGACCTCATTTCAAGACTGTTGAAGCATAATCCCAGCCAGAGGCCAATGCTCAG  
AGAAGTACTTGAACACCCCTGGATCACAGCAAATTCATCAAAACCATCAAATTGCCAAAA  
CAAAGAATCAGCTAGCAAACAGTCTTAGGAATCGTGACGGGGGAGAAATCCTTGAGCCAG  
GGCTGCCATATAACCTGACAGGAACATGCTACTGAAGTTTATTTTACCATTGACTGCTGC  
CCTCAATCTAGAACGCTACACAAGAAATATTTGTTTTACTCAGCAGGTGTGCCTTAACCT  
CCCTATTCAAGAAAGCTCCACATCAATAAACATGACACTCTGAAGTGAAAGTAGCCACGAG  
AATTGTGCTACTTATACTGGTTCATAATCTGGAGGCAAGGTTGACTGCAGCCGCCCCGT  
CAGCCTGTGCTAGGCATGGTGTCTTCACAGGAGGCAAATCCAGAGCCTGGCTGTGGGGAA  
AGTGACCACTCTGCCCTGACCCCGATCAGTTAAGGAGCTGTGCAATAACCTTCCTAGTAC  
CTGAGTGAGTGTGTAACCTTATTGGGTTGGCGAAGCCTGGTAAAGCTGTTGGAATGAGTAT  
GTGATTCTTTTTAAGTATGAAAATAAAGATATATGTACAGACTTGTATTTTTCTCTGGT  
GGCATTCCTTTAGGAATGCTGTGTGTCTGTCCGGCACCCCGGTAGGCCTGATTGGGTTTC  
TAGTCCTCCTTAACCACTTATCTCCCATATGAGAGTGTGAAAAATAGGAACACGTGCTCT  
ACCTCCATTTAGGGATTTGCTTGGGATACAGAAGAGGCCATGTGTCTCAGAGCTGTTAAG  
GGCTTATTTTTTTAAACATTGGAGTCATAGCATGTGTGTAACTTTAAATATGCAAATA  
AATAAGTATCTATGTCTAAAAA

13/46

**FIGURE 10**

MDRSKENCISGPVKATAPVGGPKRVLVTQQIPCONPLPVNSGQAQRVLCPSNSSQRVPLQ  
AQKLVSSHKPVQNKQKQLQATSVPHVSRPLNNTQKSKQPLPSAPENNPEEELASKQKN  
EESKKRQWALEDFEIGRPLGKGFVYLAAREKQSKFILALKVLFKAQLEKAGVEHQLRR  
EVEIQSHLRHPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL  
ANALSYCHSKRVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM  
IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLI  
SRLLKHNPSQRPMLREVLEHPWITANSSKPSNCONKESASKQS

N-glycosylation site.

52-55  
93-96  
386-389

cAMP- and cGMP-dependent protein kinase phosphorylation site.

285-288  
339-342

Tyrosine kinase phosphorylation site.

326-334

Serine/Threonine protein kinases active-site signature.

252-264

Protein kinase domain  
133-383

14/46

**FIGURE 11**

GGCCGGACAGTCCGCCGAGGTGCTCGGTGGAGTCATGGCAGTGCCCTTTGTGGAAGACTG  
GGACTTGGTGCAAACCTGGGAGAAGGTGCCTATGGAGAAGTTCAACTTGCTGTGAATAG  
AGTAACTGAAGAAGCAGTCGCAGTGAAGATTGTAGATATGAAGCGTGCCGTAGACTGTCC  
AGAAAATATTAAGAAAGAGATCTGTATCAATAAAATGCTAAATCATGAAAATGTAGTAAA  
ATTCTATGGTCACAGGAGAGAAGGCAATATCCAATATTTATTTCTGGAGTACTGTAGTGG  
AGGAGAGCTTTTGGACAGAATAGAGCCAGACATAGGCATGCCTGAACCAGATGCTCAGAG  
ATTCTTCCATCAACTCATGGCAGGGGTGGTTTATCTGCATGGTATTGGAATAACTCACAG  
GGATATTAAACCAGAAAATCTTCTGTTGGATGAAAGGGATAACCTCAAAATCTCAGACTT  
TGGCTTGGCAACAGTATTTCCGTATAATAATCGTGAGCGTTTGTGGAACAAGATGTGTGG  
TACTTTACCATATGTTGCTCCAGAACTTCTGAAGAGAAGAGAATTTCATGCAGAACAGT  
TGATGTTTGGTCCGTGTGGAATAGTACTTACTGCAATGCTCGCTGGAGAATTGCCATGGGA  
CCAACCCAGTGACAGCTGTCAGGAGTATTCTGACTGGAAAGAAAAAAAACATACTCAA  
CCCTTGGAaaaaaaATCGATTCTGCTCCTCTAGCTCTGCTGCATAAAATCTTAGTTGAGAA  
TCCATCAGCAAGAATTACCATTCCAGACATCAaaaaAGATAGATGGTACAACAAACCCCT  
CAAGAAAGGGGCAaaaAGGCCCGAGTCAC TTCAGGTGGTGTGTCAGAGTCTCCAGTGG  
ATTTTCTAAGCACATTCAATCCAATTTGGACTTCTCTCCAGTAAACAGTGCTTCTAGTGA  
AGAAAATGTGAAGTACTCCAGTTCTCAGCCAGAACCCCGCACAGGTCTTTCCTTATGGGA  
TACCAGCCCCCTCATACATTGATAAATTGGTACAAGGGATCAGCTTTTCCCAGCCCACATG  
TCCTGATCATATGCTTTTGAATAGTCAGTTACTTGGCACCCAGGATCCTCACAGAACCC  
CTGGCAGCGGTTGGTCAaaAGAATGACACGATTCTTTACCAAAATTGGATGCAGACAAATC  
TTATCAATGCCTGAAAGAGACTTGTGAGAAGTTGGGCTATCAATGGAAGAAAAGTTGTAT  
GAATCAGGTTACTATATCAACAAC TGATAGGAGAAACAATAAACTCATTTTCAAAGTGAA  
TTTGTTAGAAAATGGATGATAAAATATTGGTTGACTTCCGGCTTTCTAAGGGTGATGGATT  
GGAGTTCAAGAGACACTTCCTGAAGATTAAAGGGAAGCTGATTGATATTGTGAGCAGCCA  
GAAGGTTTGGCTTCCTGCCACATTCATCGGACCATCGGCTCTGGGGAATCCTGGTGAATAT  
AGTGCTGCTATGTTGACATTATTCTTCCTAGAGAAGATTATCCTGTCCTGCAAACTGCAA  
ATAGTAGTTCCCTGAAGTGTTCACTTCCCTGTTTATCCAAACATCTTCCAATTTATTTGT  
TTGTTCCGCATACAAATAATACCTATATCTTAATTGTAAGCAAACTTTGGGGAAAGGAT  
GAATAGAATTCATTTGATTATTTCTTCATGTGTGTTTAGTATCTGAATTTGAACTCATC  
TGGTGGAACCAAGTTTTCAGGGGACATGAGTTTTCCAGCTTTTATACACACGTATCTCAT  
TTTTATCAAAACATTTTGT

15/46

**FIGURE 12**

MAVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEA VAVKIVDMKRAVDCPENIKKEICINK  
MLNHENVVKFYGHRREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVVY  
LHGIGITHRDIKPENLLLDERONLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLK  
RREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKKTYLNPWKIDSAPLA  
LLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRPRVTSGGVSESPSGFSKHIQSNLDF  
SPVNSASSEENVKYSSSQPEPRTGLSLWDTSPSYIDKL VQGISFSQPTCPDHMLLNSQLL  
GTPGSSQNPWQRLVKRMTRFFTKLDADKSYQCLKETCEKLG YQWKKSCMNQVTISTDRR  
NNKLIFKVNLLLEMDDKILVDFRLSKGDGLEFKRHFLKIKGKLIDIVSSQKVWLPAT

cAMP- and cGMP-dependent protein kinase phosphorylation site.

375-378

Tyrosine kinase phosphorylation site.

383-390

394-402

N-myristoylation site.

123-128

195-200

341-346

361-366

Serine/Threonine protein kinases active-site signature.

126-138

Protein kinase domain

9-265

16/46

**FIGURE 13**

CCGCGGTTCCGGCTGCTCCGGCGAGGCGACCCTTGGGTCCGGCGCTGCGGGCGAGGTGGGC  
AGGTAGGTGGGCGGACGGCCGCGGTTCTCCGGCAAGCGCAGGCGGGGAGTCCCCACGG  
CGCCCGAAGCGCCCCCGCACCCCCGGCTCCAGCGTTGAGGCGGGGGAGTGAGGAGATG  
CCGACCCAGAGGGACAGCAGCACCATGTCACACCGGTCGCAGGCGGGCGGCAGCGGGGAC  
CATCCCACCAGGTCCGGGTGAAAGCCTACTACCGCGGGGATATCATGATAACACATTTT  
GAACCTTCCATCTCCTTTGAGGGCCTTTGCAATGAGGTTGAGACATGTGTTCTTTGAC  
AACGAACAGCTCTTCACCATGAAATGGATAGATGAGGAAGGAGACCCGTGTACAGTATCA  
TCTCAGTTGGAGTTAGAAGAAGCCTTAGACTTTATGAGCTAAACAAGGATTCTGAACTC  
TTGATTCATGTGTCCCTTGTGTACCAGAACGTCTTGGGATGCCTTGTCCAGGAGAAGAT  
AAATCCATCTACCGTAGAGGTGCACGCCGCTGGAGAAAAGCTTTATTGTGCCAATGGCCAC  
ACTTTCCAAGCCAAGCGTTTCAACAGCGCTGCTCACTGTGCCATCTGCACAGACCGAATA  
TGGGGACTTGGACGCCAAGGATATAAGTGCATCAACTGCAAACTCTTGGTTCATAAGAAG  
TGCCATAAACTCGTCACAAATTGAATGTGGGCGGCATTCTTTGCCACAGGAACCAAGTATG  
CCCATGGATCAGTCATCCATGCATTCTGACCATGCACAGACAGTAATTCATATAATCCT  
TCAAGTCATGAGAGTTTGGATCAAGTTGGTGAAGAAAAAGAGGCAATGAACACCAGGGAA  
AGTGGCAAAGCTTCATCCAGTCTAGGTCTTCAGGATTTTGATTTGCTCCGGGTAATAGGA  
AGAGGAAGTTATGCCAAAGTACTGTTGGTTCGATTAAAAAAAACAGATCGTATTTATGCA  
ATGAAAGTTGTGAAAAAAGAGCTTGTAAATGATGATGAGGATATTGATTGGGTACAGACA  
GAGAAGCATGTGTTTGAGCAGGCATCCAATCATCCTTTCTTGTGGGCTGCATTCTTGC  
TTTCAGACAGAAAGCAGATTGTTCTTTGTTATAGAGTATGTAAATGGAGGAGACCTAATG  
TTTCATATGCAGCGACAAAGAAAACCTTCTGAAGAACATGCCAGATTTTACTCTGCAGAA  
ATCAGTCTAGCATTAATTTATCTTCATGAGCGAGGGATAATTTATAGAGATTTGAACTG  
GACAATGTATTACTGGACTCTGAAGGCCACATTAACTCACTGACTACGGCATGTGTAAG  
GAAGGATTACGGCCAGGAGATACAACCAGCACTTTCTGTGGTACTCCTAATTACATTGCT  
CCTGAAATTTTAAGAGGAGAAGATTATGGTTTCAGTGTTGACTGGTGGGCTCTTGGAGTG  
CTCATGTTTGAGATGATGGCAGGAAGGTCTCCATTTGATATTGTTGGGAGCTCCGATAAC  
CCTGACCAGAACACAGAGGATTATCTCTTCCAAGTTATTTTGGAAAAACAAATTCGCATA  
CCACGTTCTCTGTCTGTAAAGCTGCAAGTGTTCTGAAGAGTTTCTTAATAAGGACCCCT  
AAGGAACGATTGGGTGTCATCTTCAAACAGGATTTGCTGATATTCAGGGACACCCGTTT  
TTCCGAAATGTTGATTGGGATATGATGGAGCAAAAACAGGTGGTACCTCCCTTTAAACCA  
AATATTTCTGGGGAATTTGGTTTGGACAACCTTTGATTCTCAGTTTACTAATGAACCTGTC  
CAGCTCACTCCAGATGACGATGACATTGTGAGGAAGATTGATCAGTCTGAATTTGAAGGT  
TTTGAGTATATCAATCCTCTTTTGATGTCTGCAGAAGAATGTGTCTGATCCTCATTTTTC  
AACCATGTATTCTACTCATGTTGCCATTTAATGCATGGATAAACTTGCTGCAAGCCTGGA  
TACAATTAACCATTTTATATTTGCCACCTACAAAAAACACCCAATATCTTCTCTGTAG  
ACTATATGAATCAATTATACATCTGTTTTACTATGAAAAAAAATTAATACTACTAGCT  
TCCAGACAATCATGTCAAAATTTAGTTGAACTGGTTTTTCAGTTTTTAAAGGCCTACAG  
ATGAGTAATGAAGTTACCTTTTTTGTTTAAAAAAAAG



17/46

**FIGURE 14**

MSHTVAGGGSGDHSQVRVKAYYRGDIMITHFEPSSISFEGLCNEVRDMCSFDNEQLFTMK  
WIDEEGDPCTVSSQLELEEAFLRYELNKDSELLIHVFPCVPERPGMPCPGEDKSIYRRGA  
RRWRKLYCANGHTFQAKRFNRRHAICAICTDRIWGLGRQGYKCINCKLLVHKKCHKLV  
TIE CGRHSPLQEPVMPMDQSSMHS DHAQTVIPYNPSSHESLDQVGEEKEAMNTRESGKASSSL  
GLQDFDLLRVIGRGSYAKVLLVRLKKTDRYAMKVVKELVNDDDEDIDWVQTEKHVFEQA  
SNHPFLVGLHSCFQTESRLFFVIEYVNGGDLMFHMQRQRKLPEEHARFYSAEISLALNYL  
HERGIYRDLKLDNVLLDSEGHKLT DYGMCKEGLRPGDTTSTFCGTPNYIAPEILRGED  
YGFSDWWALGVLMFEMMAGRSPFDIVGSSDNDPDQNTEDYLEQVILEKQIRIPRSLSVKA  
ASVLKSFLNKDPKERLGCHPQTGFADIQGHPPFRNVWDMMEQKQVVPFVKPNISGEFGL  
DNFDSQFTNEPVQLTPDDDDIVRKIDQSEFEGFEYINPLLMSAECEV

N-glycosylation site.

533-536

Tyrosine kinase phosphorylation site.

265-271

N-myristoylation site.

7-12  
308-313  
394-399

Cell attachment sequence.

24-26

Serine/Threonine protein kinases active-site signature.

365-377

Protein kinase domain  
245-513

Protein kinase C terminal domain  
514-580

Phorbol esters/diacylglycerol binding domain  
132-181

Octicosapeptide repeat  
56-85

18/46

**FIGURE 15**

GC GGCGGGCGGGCGGCAGTTTGCTCATACTTTGTGACTTGCGGTACAGTGGCATTTCAGC  
TCCACACTTGGTAGAACACAGGCACGACAAGCATAGAAACATCCTAAACAATCTTCATC  
GAGGCATCGAGGTCCATCCCAATAAAAATCAGGAGACCCTGGCTATCATAGACCTTAGTC  
TTCGCTGGTATACTCGCTGTCTGTCAACCAGCGGTTGACTTTTTTTAAGCCTTCTTTTTT  
CTCTTTTACAGTTTCTGGAGCAAATTCAGTTTGCCTTCCTGGATTTGTAAATTGTAATG  
ACCTCAAACTTTAGCAGTTCTTCCATCTGACTCAGGTTTGCTTCTCTGGCGGTCTTCAG  
AATCAACATCCACACTTCCGTGATTATCTGCGTGCATTTTGGACAAAGCTTCCAACCAGG  
ATACGGGAAGAAGAAATGGCTGGTGATCTTTCAGCAGGTTTCTTCATGGAGGAACCTTAAT  
ACATACCGTCAGAAGCAGGGAGTAGTACTTAAATATCAAGAAGTGCCTAATTCAGGACCT  
CCACATGATAGGAGGTTTACATTTCAAGTTATAATAGATGGAAGAGAATTTCCAGAAGGT  
GAAGGTAGATCAAAGAAGGAAGCAAAAAATGCCGCAGCCAAATTAGCTGTTGAGATACTT  
AATAAGGAAAAGAAGGCAGTTAGTCCCTTTATTATTGACAACAACGAATTCCTCAGAAGGA  
TTATCCATGGGGAAATTACATAGGCCCTTATCAATAGAATTGCCCAGAAGAAAAGACTAACT  
GTAATTTATGAACAGTGTGCATCGGGGGTGCATGGGCCAGAAGGATTTCAATTATAAATGC  
AAAATGGGACAGAAAAGAAATATAGTATTGGTACAGGTTCTACTAAACAGGAAGCAAAACAA  
TTGGCCGCTAAACTTGCATATCTTCAGATATTATCAGAAGAAACCTCAGTGAAATCTGAC  
TACCTGTCTCTGGTCTTTTTGCTACTACGTGTGAGTCCCAAAGCAACTCTTTAGTGACC  
AGCACACTCGCTTCTGAATCATCATCTGAAGGTGACTTCTCAGCAGATACATCAGAGATA  
AATTTCTAACAGTGACAGTTTAAACAGTTCTTCGTTGCTTATGAATGGTCTCAGAAATAAT  
CAAAGGAAGGCAAAAGATCTTTGGCACCCAGATTTGACCTTCCTGACATGAAAGAAACA  
AAGTATACTGTGGACAAGAGGTTTGGCATGGATTTTAAAGAAATAGAATTAATTGGCTCA  
GGTGGATTTGGCCAGTTTTCAAAGCAAAACACAGAATTGACGGAAAGACTTACGTTATT  
AAACGTGTTAAATATAATAACGAGAAGGCGGAGCGTGAAGTAAAAGCATTGGCAAAACTT  
GATCATGTAAATATTGTTCACTACAATGGCTGTTGGGATGGATTTGATTATGATCCTGAG  
ACCAGTGATGATTCTCTTGAGAGCAGTGATTATGATCCTGAGAACAGCAAAAATAGTTCA  
AGGTCAAAGACTAAGTGCTTTTTCATCCAAATGGAATTCCTGTGATAAAGGGACCTTGGAA  
CAATGGATTGAAAAAAGAAGAGGCGAGAAACTAGACAAAGTTTTGGCTTTGGAACCTCTT  
GAACAAATAACAAAAGGGGTGGATTATATACATTCAAAAAATTAATTCATAGAGATCTT  
AAGCCAAAGTAATATATTCTTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTT  
GTAACATCTCTGAAAAATGATGGAAAGCGAACAAAGGAGTAAGGGAACTTTGCGATACATG  
AGCCCAAGACAGATTTCTTCGCAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGG  
CTAATTTCTTGCTGAACCTTCTTCATGTATGTGACACTGCTTTTGAAACATCAAAGTTTTTC  
ACAGACCTACGGGATGGCATCATCTCAGATATATTTGATAAAAAAGAAAAAATCTTCTA  
CAGAAATTACTCTCAAAGAAACCTGAGGATCGACCTAACACATCTGAAATACTAAGGACC  
TTGACTGTGTGGAAGAAAAGCCCAGAGAAAAATGAACGACACACATGTTAGAGCCCTTCT  
GAAAAAGTATCCTGCTTCTGATATGCAGTTTTCTTAAATTATCTAAAATCTGCTAGGGA  
ATATCAATAGATATTTACCTTTTTATTTTAAATGTTTCCTTTAATTTTTTACTATTTTACT  
AATCTTTCTGCAGAAACAGAAAGGTTTTCTTCTTTTTTGTCTTCAAAAACATTCTTACATTT  
TACTTTTTCTGGCTCATCTCTTATTCTTTTTTTTTTTTAAAGACAGAGTCTCGCTC  
TGTGCCCAGGCTGGAGTGCAATGACACAGTCTTGCTCACTGCAACTTCTGCTCTTGG  
GTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGATTACAGGCATGTGCCACCC  
ACCCAATAATTTTTGTGTTTTTAATAAAGACAGGGTTTTACCATGTTGGCCAGGCTGGT  
CTCAAACCTCCTGACCTCAAGTAATCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACA  
GGGATGAGCCACCGCGCCAGCCTCATCTCTTTGTTCTAAAGATGGAAAAACCCGCCA  
AATTTTCTTTTTTATACTATTAATGAATCAATCAATTCATATCTATTTATTAATTTCTAC  
CGCTTTTAGGCCAAAAAATGTAAGATCGTTCTCTGCCTCACATAGCTTACAAGCCAGCT  
GGAGAAATATGGTACTCATTAATAAAAAAAAAAAGTGATGTACAACC

19/46

**FIGURE 16**

MAGDLSAGFFMEELNTYRQKGQGVVLKYQELPNSGPPHRRFTFQVIIDGREFPEGEGRSK  
KEAKNAAAKLAVEILNKEKKAVSPLLLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQ  
CASGVHGPGEFHYKCKMGQKEYSIGTGSTKQEAQQLAAKLAYLQILSEETSVKSDYLSSG  
SFATTCESQSNLVTSTLASESSSEGDFSADTSEINSNSDSLNSSSLLMNGLRNNQRKAK  
RSLAPRFDLPDMKETKYTVDKRFGMDFKEIELIGSGGFGQVFKAKHRIDGKTYVIKRVKY  
NNEKAEREVKALAKLDHVNIVHYNGCWDGFDYDPETSDDSLESSDYDPENSKNSSRSKTK  
CLFIQMEFCDKGTLEQWIEKRRGEKLDKVLALELFEQITKGVDYIHSKKLIHRDLKPSNI  
FLVDTKQVKIGDFGLVTSKNDGKRTRSKGTLRYMSPEQISSQDYGKEVDLYALGLILAE  
LLHVCDTAFETSKFFTDLRDGIISDIFDKKEKTLQKLLSKKPEDRPNTSEILRTLTVWK  
KSPEKNERHTC

N-glycosylation site.

91-94  
223-226  
353-356  
528-531

cAMP- and cGMP-dependent protein kinase phosphorylation site.

39-42  
112-115

Tyrosine kinase phosphorylation site.

285-293

N-myristoylation site.

95-100  
99-104  
145-150  
180-185  
231-236  
325-330  
434-439  
475-480

Amidation site.

442-445

Serine/Threonine protein kinases active-site signature.

410-422

Protein kinase domain

267-538

Double-stranded RNA binding motif

10-75  
101-165

20/46

**FIGURE 17**

ATGTCTCGGGAGTCGGATGTTGAGGCTCAGCAGTCTCATGGCAGCAGTGCCTGTTACACAG  
CCCCATGGCAGCGTTACCCAGTCCCAAGGCTCCTCCTCACAGTCCCAGGGCATATCCAGC  
TCCTCTACCAGCACGATGCCAACTCCAGCCAGTCCTCTCACTCCAGCTCTGGGACACTG  
AGTCCTTAGAGACAGTGTCCACTCAGGAACCTCTATTCTATTCTGAGGACCAAGAACCT  
GAGGACCAAGAACCTGAGGAGCCTACCCCTGCCCCCTGGGCTCGATTATGGGCCCTTCAG  
GATGGATTTGCCAATCTTGAATGTGTGAATGACAACACTGGTTTGGGAGGGACAAAAGC  
TGTGAATATTGCTTTGATGAACCACTGCTGAAAAGAACAGATAAAATACCGAACATACAGC  
AAGAAACACTTTTCGGATTTTCAGGGAAGTGGGTCTAAAACTCTTACATTGCATACATA  
GAAGATCACAGTGGCAATGGAACCTTTGTAAATACAGAGCTTGTAGGGAAAGGAAAACGC  
CGTCCTTTGAATAACAATTCTGAAATTGCACTGTCACTAAGCAGAAATAAAGTTTTTGTC  
TTTTTTGATCTGACTGTAGATGATCAGTCAGTTTATCCTAAGGCATTAAGAGATGAATAC  
ATCATGTCAAAAACCTCTTGGAAGTGGTGCCTGTGGAGAGGTAAAGCTGGCTTTTCGAGAGG  
AAAACATGTAAGAAAGTAGCCATAAAGATCATCAGCAAAAGGAAGTTTGCTATTGGTTCA  
GCAAGAGAGGCAGACCCAGCTCTCAATGTTGAAACAGAAATAGAAATTTTGAAAAAGCTA  
AATCATCCTTGCATCATCAAGATTAAAACTTTTTTTGATGCAGAAGATTATTATATTGTT  
TTGGAATTGATGGAAGGGGGAGAGCTGTTTGACAAAGTGGTGGGGAATAAACGCCTGAAA  
GAAGCTACCTGCAAGCTCTATTTTTACCAGATGCTCTTGGCTGTGCAGTACCTTCATGAA  
AACGGTATTATACACCGTGACTTAAAGCCAGAGAATGTTTTACTGTCATCTCAAGAAGAG  
GACTGTCTTATAAAGATTACTGATTTTGGGCACTCCAAGATTTTGGGAGAGACCTCTCTC  
ATGAGAACCTTATGTGGAACCCCCACCTACTTGGCGCCTGAAGTTCTTGTCTGTTGGG  
ACTGCTGGGTATAACCGTGCTGTGGACTGCTGGAGTTTAGGAGTTATTCTTTTTATCTGC  
CTTAGTGGGTATCCACCTTTCTCTGAGCATAGGACTCAAGTGTCACTGAAGGATCAGATC  
ACCAGTGGAAAATACAACCTTCATTCCCTGAAGTCTGGGCAGAAGTCTCAGAGAAAGCTCTG  
GACCTTGTCAGAAGTTGTTGGTAGTGGATCCAAAGGCACGTTTTACGACAGAAGAAGCC  
TTAAGACACCCGTGGCTTCAGGATGAAGACATGAAGAGAAAGTTTCAAGATCTTCTGTCT  
GAGGAAAATGAATCCACAGCTCTACCCCAGGTTCTAGCCCAGCCTTCTACTAGTCGAAAG  
CGGCCCCGTGAAGGGGAAGCCGAGGGTGCCGAGACCACAAAGCGCCAGCTGTGTGTGCT  
GCTGTGTTGTGAACTCCGTGGTTTGAACACGAAAGAAATGTCCTTCTTTCACTCTGCATC  
TTTCTTTTCTTTGAGTCGTTTTTTTATAGTTGGATTTAATTATGGAATAATGGTTT

21/46

**FIGURE 18**

MSRES DVEAQQSHGSSACSQPHGSVTQSQGSSSSQSGISSSSSTSTMPNSSQSSHSSSGTL  
SSLETVSTQELYSIPE DQEPEDQEP EPT PAPWARLWALQDGFANLECVNDNYWFG RDKS  
CEYCFDEPLLKRTDKYRTYSKKHFRI FREVGPKN SYIAYIEDHSGNGTFVNTELVGKGKR  
RPLNNNSEIALSLSRNKVFFFDLTVD DQSVYPKALRDEYIMSKTLGSGACGEVKLA FER  
KTCKKVAIKIISKRKFAIGSAREADPALNVETEIEILKKLNHP CIIKIKNFFDAEDYYIV  
LELMEGGELFDKVVG NKRLEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQEE  
DCLIKITDFGH SKILGETSLMRTL CGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFIC  
LSGYPPFSEHRTQVSLKDQITSGKYNF IPEVWAEVSEKALDLVKKLLVVD PKARFTTEEA  
LRHPWLQDEDMKRKFQDLLSEENESTALPQVLAQPSTSRKRPREGEAEGAETTKRPAVCA  
AVL

N-glycosylation site.

48-51  
166-169  
185-188  
503-506

Glycosaminoglycan attachment site.

164-167

Tyrosine kinase phosphorylation site.

289-297

N-myristoylation site.

14-19  
37-42  
58-63  
167-172  
227-232  
529-534

Amidation site.

177-180

Serine/Threonine protein kinases active-site signature.

343-355

Protein kinase domain

220-486

FHA domain

113-192

22/46

**FIGURE 19**

GGCACGAGTAGGGGTGGCGGGTCAGTGCTGCTCGGGGGCTTCTCCATCCAGGTCCCTGGA  
GTTCCCTGGTCCCTGGAGCTCCGCACTTGGCGCGCAACCTGCGTGAGGCAGCGCGACTCTG  
GCGACTGGCCGGCCATGCTTCCCGGGCTGAGGACTATGAAGTGTTGTACACCATTTGGCA  
CAGGCTCCTACGGCCGCTGCCAGAAGATCCGGAGGAAGAGTGATGGCAAGATATTAGTTT  
GGAAAGAACTTGACTATGGCTCCATGACAGAAGCTGAGAAACAGATGCTTGTCTGAAG  
TGAATTTGCTTCGTGAACGAAACATCCAAACATCGTTCGTTACTATGATCGGATTATTG  
ACCGGACCAATACAACACTGTACATTGTAATGGAATATTGTGAAGGAGGGGATCTGGCTA  
GTGTAATTACAAAGGGAACCAAGGAAAGGCAATACTTAGATGAAGAGTTTGTCTTCGAG  
TGATGACTCAGTTGACTCTGGCCCTGAAGGAATGCCACAGACGAAGTGATGGTGGTCATA  
CCGTATTGCATCGGGATCTTAAACCAGCCAATGTTTTCCTGGATGGCAAGCAAAACGTCA  
AGCTTGGAGACTTTGGGCTAGCTAGAATATTAACCATGACACGAGTTTTCGCAAAAACAT  
TTGTTGGCACACCTTATTACATGTCTCCTGAACAAATGAATCGCATGTCTACAATGAGA  
AATCAGATATCTGGTCATTGGGCTGCTTGCTGTATGAGTTATGTGCATTAATGCCTCCAT  
TTACAGCTTTTAGCCAGAAAGAACTCGCTGGGAAAATCAGAGAAGGCAAATTCAGGCGAA  
TTCCATACCGTTACTCTGATGAATTGAATGAAATTATTACGAGGATGTTAACTTAAAGG  
ATTACCATCGACCTTCTGTTGAAGAAATTCTTGAGAACCCTTTAATAGCAGATTGGTTG  
CAGACGAGCAAAGAAGAAATCTTGAGAGAAGAGGGCGACAATTAGGAGAGCCAGAAAAAT  
CGCAGGATTCCAGCCCTGTATTGAGTGAGCTGAACTGAAGGAAATTCAGTTACAGGAGC  
GAGAGCGAGCTCTCAAAGCAAGAGAAGAAAGATTGGAGCAGAAAGAACAGGAGCTTTGTG  
TTCGTGAGAGACTAGCAGAGGACAACTGGCTAGAGCAGAAAAATCTGTTGAAGAACTACA  
GCTTGCTAAAGGAACGGAAGTTCTGTCTCTGGCAAGTAATCCAGAACTTCTTAATCTTC  
CATCCTCAGTAATTAAGAAGAAAGTTCAATTTAGTGGGGAAAGTAAAGAGAACATCATGA  
GGAGTGAGAATTCTGAGAGTCAGCTCACATCTAAGTCCAAGTGCAAGGACCTGAAGAAAA  
GGCTTCACGCTGCCAGCTGCGGGCTCAAGCCCTGTCAGATATTGAGAAAAATTACCAAC  
TGAAAGCAGACAGATCCTGGGCATGCGCTAGCCAGGTAGAGAGACACAGAGCTGTGTAC  
AGGATGTAATATTACCAACCTTTAAAGACTGATATTCAAATGCTGTAGTGTTGAATACTT  
GGCCCCATGAGCCATGCCTTTCTGTATAGTACACATGATATTTCCGAATTGGTTTTACTG  
TTCTTCAGCAACTATTGTACAAAATGTTACATTTAATTTTTCTTTCTTTTAAAGAAC  
ATATTATAAAAAGAATACTTTCTTGTTGGGCTTTTAACTCTGTGTGTGATTACTAGTAG  
GAACATGAGATGTGACATTCTAAATCTTGGGAGAAAAATAATATTAGGAAAAAAATATT  
TATGCAGGAAGAGTAGCACTCACTGAATAGTTTTAAATGACTGAGTGGTATGCTTACAAT  
TGTCATGTCTAGATTTAAATTTTAAAGTCTGAGATTTTAAATGTTTTTGAGCTTAGAAAAC  
CCAGTTAGATGCAATTTGGTCATTAATACCATGACATCTTGCTTATAAATATTCCATTGC  
TCTGTAGTTCAAATCTGTTAGCTTTGTGAAAATTCATCACTGTGATGTTTGTATTCTTTT  
TTTTTTCTGTTTAAACAGAATATGAGCTGTCTGTCATTTACCTACTTCTTTCCCACTAAA  
TAAAAGAATTCTTCAGTTA

23/46

**FIGURE 20**

MPSRAEDYEVLYTIGTGSYGRQCQKIRRKSDGKILVWKELDYGSMTEAEKQMLVSEVNLLR  
ELKHPNIVRYDRIIDRTNTTLYIVMEYCEGGDLASVITKGTKERQYLDEEFVLRVMTQL  
TLALKECHRRSDGGHTVLHRDLKPANVFLDGKQNVKLGDGFLARILNHDTSFAKTFVGTP  
YYMSPEQMNRMSSYNEKSDIWSLGCCLLYELCALMPPTAFSOKELAGKIREGKFRRIPYRY  
SDELNEIITRMLNLKDYHRPSVEEILENPLIADLVADEQRRNLERRGRQLGEPEKSQDSS  
PVLSELKLKEIQLERERALKAREERLEQKEQELCVRRERLAEDKLARAENLLKNYSLLKE  
RKFLSLASNPELLNLPSSVIKKKVHFSGESKENIMRSENSESQLTSSKCKDLKKRLHAA  
QLRAQALS DIEKNYQLKSRQILGMR

N-glycosylation site.

79-82  
354-357

cAMP- and cGMP-dependent protein kinase phosphorylation site.

26-29

Tyrosine kinase phosphorylation site.

100-107

N-myristoylation site.

91-96

Leucine zipper pattern.

306-327  
313-334

Serine/Threonine protein kinases active-site signature.

137-149

Protein kinase domain

8-271

24/46

**FIGURE 21**

TTGGCGGGCGGAAGCGGCCACAACCCGGCGATCGAAAAGATTCTTAGGAACGCCGTACCA  
GCCGCGTCTCTCAGGACAGCAGGCCCTGTCTTCTGTGCGGGCGCCGCTCAGCCGTGCC  
TCCGCCCTCAGGTTCTTTTTCTAATTCCAAATAAACTTGCAAGAGGACTATGAAAAGATT  
ATGATGAACTTCTCAAATATTATGAATTACATGAACTATTGGGACAGGTGGCTTTGCAA  
AGGTCAAACCTTGCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAAATCATGGATA  
AAAACACACTAGGGAGTGATTTGCCCCGGATCAAAACGGAGATTGAGGCCTTGAAGAACC  
TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGACAGCCAACAAAATATTCA  
TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCAGGATCGCC  
TGTCAGAAGAGGAGACCCGGGTGTCTTCCGTCAGATAGTATCTGCTGTTGCTTATGTGC  
ACAGCCAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAATTTGCTGTTTGATGAATATC  
ATAAATTAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAAGGGTAACAAGGATTACC  
ATCTACAGACATGCTGTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATACAAGGCAAAT  
CATATCTTGGATCAGAGGCAGATGTTTGGAGCATGGGCATACTGTTATATGTTCTTATGT  
GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAAGAAGATTATGAGAG  
GAAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTCTGCTTCTTCAACAAATGC  
TGCAGGTGGACCCAAAGAAACGGATTTCTATGAAAATCTATTGAACCATCCCTGGATCA  
TGCAAGATTACAACATATCCTGTTGAGTGGCAAAGCAAGAATCCTTTTATTCACCTCGATG  
ATGATTGCGTAACAGAACCTTTCTGTACATCACAGAAACAACAGGCAAACAATGGAGGATT  
TAATTTCACTGTGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTTCTAGCCAAGA  
AGGCTCGGGGAAAACCAAGTTCGTTTAAGGCTTTCTTCTTTCTCCTGTGGACAAGCCAGTG  
CTACCCCATTCACAGACATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGTG  
ATAAAAATTATGTGGCGGGATTAATAGACTATGATTGGTGTGAAGATGATTTATCAACAG  
GTGCTGCTACTCCCCGAACATCACAGTTTACCAAGTACTGGACAGAATCAAATGGGGTGG  
AATCTAAATCATTAACTCCAGCCTTATGCAGAACACCTGCAAATAAATTAAAGAACAAG  
AAAATGTATATACTCCTAAGTCTGCTGTAAAGAATGAAGAGTACTTTATGTTTCTTGAGC  
CAAAGACTCCAGTTAATAAGAACCAGCATAAGAGAGAAATACTCACTACGCCAAATCGTT  
ACACTACACCCTCAAAGCTAGAAACCAGTGCCTGAAAGAACTCCAATTAATAATACCAG  
TAAATTCAACAGGAACAGACAAGTTAATGACAGGTGTCATTAGCCCTGAGAGGCGGTGCC  
GCTCAGTGGAATTGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAAGAAAGGGAG  
CCAAAGTGTGTTGGGAGCCTTGAAAGGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA  
GCAAAAGGAAGGGTTCTGCCAGAGACGGGCCAGAAAGACTAAAGCTTCACTATAATGTGA  
CTACAAC TAGATTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATTCTTCCAA  
AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAACACAGTCAGATT  
TTGGGAAAGTGACAATGCAATTTGAATTAGAAGTGTGCCAGCTTCAAAAACCCGATGTGG  
TGGGTATCAGGAGGCAGCGGCTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGGAAG  
ACATCCTATCTAGCTGCAAGGTATTAATTGATGGATTCTTCCATCCTGCCGGATGAGTGTG  
GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA  
CTACCAACTTGTGTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAA  
GATATTATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCATTATGTTACTGTCTTTTT  
TAATCATGTGGTTTTGTATATTAATAATTGTTGACTTCTTAGATTCACTTCCATATGTG  
AATGTAAGCTCTTAACATATGTCTCTTTGTAATGTGTAATTTCTTTCTGAAATAAACCAT  
TTGTGAATAT



25/46

**FIGURE 22**

MKDYDELLKYYELHETIGTGGFACVVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA  
LKNLRHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEEETRVVFRQIVSAV  
AYVHSQGYAHRDLKPENLLFDEYHKLKLI DFGLCAKPKGNKDYLQTCCGSLAYAAPELI  
QGKSYLGSEADVWSMGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPKWLSPPSSILL  
QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFHLDODDCVTELSVHHRNNRQT  
MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSSFSCGQASATPFTDIKSNNWSLEDV  
TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALC RTPANKL  
KNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI  
KIPVNSTGTDKLMTGVISPERRCRSVELDLNQAHEETPKRKGAKVFGSLERGLDKVITV  
LTRSKRKGSARDGPRRLKHLHYNVTTRLVNPDQLLNEIMSILPKKHVDFVQKGYTLKCQT  
QSDFGKVTMQFELEVCQLQKPDVVGI RRQLKGDWVYKRLVEDILSSCKV

N-glycosylation site.

354-357  
485-488  
562-565

cAMP- and cGMP-dependent protein kinase phosphorylation site.

250-253  
546-549

Tyrosine kinase phosphorylation site.

2-10  
421-427  
630-638

N-myristoylation site.

340-345

Microbodies C-terminal targeting signal.

649-652

Leucine zipper pattern.

165-186

Serine/Threonine protein kinases active-site signature.

128-140

Protein kinase domain

11-263

Kinase associated domain 1

602-651

26/46

**FIGURE 23**

GTCTTTATTTTTCAGTCCCGGATCCGCGGGCGCAGGCCAGCTCAGGCCCCAGGGATGGAC  
GTCGTGGACCTGACATTTTCAATAGAGACCCCGGGACCCTATGACCTGCTACAGCGG  
CTGGGTGGCGGCACGTATGGGGAAGTCTTTAAGGCTCGAGACAAGGTGTCAGGGGACCTG  
GTGGCACTGAAGATGGTGAAGATGGAGCCTGATGATGATGTCTCCACCCTTCAGAAGGAA  
ATCCTCATATTGAAAACCTTGCCGGCACGCCAACATCGTGGCCTACCATGGGAGTTATCTC  
TGGTTGCAGAACTCTGGATCTGCATGGAATTCTGTGGGGCTGGTTCTCTCCAGGACATC  
TACCAAGTGACAGGCTCCCTGTCAGAGCTCCAGATTAGCTATGTCTGCCGGGAAGTGCTC  
CAGGGACTGGCCTATTTGCACTCACAGAAGAAGATACACAGGGACATCAAGGGAGCTAAC  
ATCCTCATCAATGATGCTGGGGAGGTGAGATTGGCTGACTTTGGCATCTCGGCCAGATT  
GGGGCTACACTGGCCAGACGCCTCTCTTTCATTGGGACACCCTACTGGATGGCTCCGGAA  
GTGGCAGCTGTGGCCCTGAAGGGAGGATACAATGAGCTGTGTGACATCTGGTCCCTGGGC  
ATCACGGCCATCGAACTGGCCGAGCTACAGCCACCGCTCTTTGATGTGCACCCTCTCAGA  
GTTCTCTTCTCATGACCAAGAGTGGCTACCAGCCTCCCCGACTGAAGGAAAAAGGCAAA  
TGGTCGGCTGCCCTCCACAACCTTCATCAAAGTCACTCTGACTAAGAGTCCCAAGAAACGA  
CCCAGCGCCACCAAGATGCTCAGTCATCAACTGGTATCCCAGCCTGGGCTGAATCGAGGC  
CTGATCCTGGATCTTCTTGACAACTGAAGAATCCCGGGAAAGGACCCTCCATTGGGGAC  
ATTGAGGATGAGGAGCCCGAGCTACCCCTGCTATCCCTCGGCGGATCAGATCCACCCAC  
CGCTCCAGCTCTCTGGGGATCCCAGATGCAGACTGCTGTGCGGCGGCACATGGAGTTCAGG  
AAGCTCCGAGGAATGGAGACCAGACCCCGAGCCAACACCGCTCGCCTACAGCCTCCTCGA  
GACCTCAGGAGCAGCAGCCCCAGGAAGCAACTGTGAGAGTCGTCTGACGATGACTATGAC  
GACGTGGACATCCCCACCCCTGCAGAGGACACACCTCCTCCACTTCCCCCAAGCCCAAG  
TTCCGTTCTCCATCAGACGAGGGTCTGAGGAGCATGGGGGATGATGGGCAGCTGAGCCCG  
GGGGTGCTGGTCCGGTGTGCCAGTGGGCCCCACCAAACAGCCCCCGTCTGGGGCTCCC  
CCATCCACAGCAGCCCCACCTCACCGCCCATTCAGAACCCTCACTCTGGAACCCACCC  
TCCCGGGAGCTTGACAAGCCCCACTTCTGCCCCCAAGAAGGAAAAGATGAAGAGAAAAG  
GGATGTGCCCTTCTCGTAAAGTTGTTCAATGGCTGCCCCCTCCGGATCCACAGCACGGCC  
GCCTGGACACATCCCTCCACCAAGGACCAGCACCTGCTCCTGGGGGAGAGGAAGGCATC  
TTCATCCTGAACCGAATGACCAGGAGGCCACGCTGGAAATGCTCTTCTCTAGCCGGACT  
ACGTGGGTGTACTCCATCAACAACGTTCTCATGTCTCTCTCAGGAAAGACCCCCACCTG  
TATTCTCATAGCATCCTTGGCCTGCTGGAACGGAAGAGACCAGAGCAGGAACCCCATC  
GCTCACATTAGCCCCACCGCCTACTGGCAAGGAAGAACATGGTTTCCACCAAGATCCAG  
GACACCAAAGGCTGCCGGGCGTGCTGTGTGGCGGAGGGTGCAGGCTCTGGGGGCCCGTTC  
CTGTGCGGTGCATTGGAGACGTCCGTTGTCTGCTTTCAGTGGTACCAGCCCATGAACAAA  
TTCCTGCTTGTCCGGCAGGTGCTGTTCCCACTGCCGACGCCTCTGTCCGTGTTTCGCGCTG  
CTGACCGGGCCAGGCTCTGAGCTGCCCGCTGTGTGCATCGGCGTGAGCCCCGGGCGGCCG  
GGGAAGTCGGTGCTCTTCCACACGGTGCGCTTTGGCGCGCTCTCTTGCTGGCTGGGCGAG  
ATGAGCACCGAGCACAGGGGACCCGTGCAGGTGACCCAGGTAGAGGAAGATATGGTGATG  
GTGTTGATGGATGGCTCTGTGAAGCTGGTGACCCCGAGGGGTCCCCAGTCCGGGGACTT  
CGCACACCTGAGATCCCCATGACCGAAGCGGTGGAGGCCGTGGCTATGGTTGGAGGTGAG  
CTTCAGGCCTTCTGGAAGCATGGAGTGCAGGTGTGGGCTCTAGGCTCGGATCAGCTGCTA  
CAGGAGCTGAGAGACCTACCTTCTTCCGCTGCTTGGCTCCCCCAGGCTGGAGTGC  
AGTGGCACGATCTCGCCTCACTGCAACCTCCTCCTCCAGGTTCAAGCAATTCTCCTGCC  
TCAGCCTCCCGAGTAGCTGGGATTACAGGCCTGTAGTGGTGGAGACACGCCAGTGGATG  
ATCCTACTGCTCCAGCAACCTCTACATCCAGGAATGAGTCCCTAGGGGGGTGTGAGGAA  
CTAGTCCTTGACCCCCCTCCCCATAGACACACTAGTGGTCATGGCATGTCTCATCTCC  
CAATAAACATGACTTTAGCCTCTGCAAAAAA

27/46

**FIGURE 24**

MDVVDPDIFNRDPRDHYDLLQRLGGGTYGEVFKARDKVS GDLVALKMVKMEPDDDDVSTLQ  
KEILILKTCR HANIVAYHGSYLWLQKLWICMEFCGAGSLQDIYQVTGSLSELQISYVCRE  
VLQGLAYLHSQKKIHRDIKGANILINDAGEVRLADFGISAQIGATLARRLSFIGTPYWMA  
PEVAVALKGGYNELCDIWSLGITAIELAELOPPLFDVHPLRVLFMLTKSGYQPPRLKEK  
GKWSAAFHNFIKVTLTSPKKRPSATKMLSHQLVSPGLNRGLILDLLDKLKNPGKGPSI  
GDIEDEEPELPPAIPRRIRSTHRSSSLGIPDADCCRRHMEFRKL RGMETRPPANTARLQP  
PRDLRSSSPRKQLSESSDDDDYDDVDIPTPAEDTPPPLPPKPKFRSPSDEGPGSMGDDGQL  
SPGVLVRCASGPPPNSPRPGPPPSTSSPHLTAHSEPSLWNPPSRELDKPPLLPPKKEKMK  
RKGCALLVKLFNGCPLRIHSTAATHPSTKDQHLLLGAEEGIFILNRNDQEATLEMLEPS  
RTTWVYSINNVLMSLSGKTPHLYSHSILGLLERKETRAGNP IAHISPHRLLARKNMVSTK  
IQDTKGCRACCVAEGASSGGPFLCGALETSSVLLQWYQPMNKFLLV RQVLFPLPTPLSVF  
ALLTGPGSELPAVCIGVSPGRPGKSVLFHTVRFGALSCWL GEMSTEHRGPVQVTQVEEDM  
VMVLMDGSVKLVTPEGSPVRGLRTP EIPMTEAVEAVAMVGGQLQAFWKHGVQVWALGSDQ  
LLQELRDP TLTFRLLGSPRLECSGTISPHCNLLLPGSSNSPASASRVAGITGL

cAMP- and cGMP-dependent protein kinase phosphorylation site.

168-171  
261-264  
573-576

N-myristoylation site.

25-30  
163-168  
278-283  
328-333  
517-522  
579-584  
606-611  
615-620  
625-630  
676-681  
694-699  
761-766

CNH domain  
500-805

Protein kinase domain

17-274

28/46

**FIGURE 25**

GAATTCGGCACGAAGGAGAGTAGCAGTGCCTTGGACCCCAGCTCTCCTCCCCCTTTCTCT  
CTAAGGATCGCCCCAGAAGGAGAACTCCTACCCCTGGCCCTACGGCCGACAGACGGCTCCA  
TCTGGCCTGAGCACCTGCCCCAGCGAGTCCTCCGGAAAGAGCCTGTCACCCCATCTGCA  
CTTGTCCTCATGAGCCGCTCCAATGTCCAGCCCACAGCTGCCCCCTGGCCAGAAGGTGATG  
GAGAATAGCAGTGGGACACCCGACATCTTAACGCGGCACTTCACAATTGATGACTTTGAG  
ATTGGGCGTCTCTGGGCAAAGGCAAGTTTGGAAACGTGTACTTGGCTCGGGAGAAGAAA  
AGCCATTTTCATCGTGGCGCTCAAGGTCCTCTTCAAGTCCCAGATAGAGAAGGAGGGCGTG  
GAGCATCAGCTGCGCAGAGAGATCGAAATCCAGGCCACCTGCACCATCCCAACATCCTG  
CGTCTCTACAACATATTTTTATGACCGGAGGAGGATCTACTTGATTCTAGAGTATGCCCC  
CGCGGGGAGCTCTACAAGGAGCTGCAGAAGAGCTGCACATTTGACGAGCAGCGAACAGCC  
ACGATCATGGAGGAGTTGGCAGATGCTCTAATGTACTGCCATGGGAAGAAGGTGATTCAC  
AGAGACATAAAGCCAGAAAATCTGCTCTTAGGGCTCAAGGGAGAGCTGAAGATTGCTGAC  
TTCGGCTGGTCTGTCCATGCGACCTCCCTGAGGAGGAAGACAATGTGTGGCACCTGGAC  
TACCTGCCCCCAGAGATGATTGAGGGGCGCATCGACAATGAGAAGGTGGATCTGTGGTGC  
ATTGGAGTGCTTTGCTATGAGCTGCTGGTGGGGAACCCATTTGAGAGTGCATCACACAAC  
GAGACCTATCGCCGCATCGTCAAGGTGGACCTAAAGTTCCCGCTTCTGTGCCCCACGGGA  
GCCCAGGACCTCATCTCCAACTGCTCAGGCATAACCCCTCGGAACGGCTGCCCCTGGCC  
CAGGTCTCAGCCCACCTTGGGTCCGGGCCAACTCTCGGAGGGTGCTGCCTCCCTCTGCC  
CTTCAATCTGTGCGCTGATGGTCCCTGTCATTCACTCGGGTGCGTGTGTTTGTATGTCTG  
TGTATGTATAGGGGAAAGAAGGGATCC

29/46

**FIGURE 26**

MAQKENSYPWPYGRQTAPSGLSTLPQRVLRKEPVTPSALVLMRSRNVQPTAAPGQKVMEN  
SSGTPDILTRHFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVEH  
QLRREIEIQAHLHHPNILRLYNFYDRRIYLLILEYAPRGELYKELQKSCTFDEQRTATI  
MEELADALMYCHGKKVIHRDIKPENLLLGLKGELKIADFGWSVHATSLRRKTMCGTLDYL  
PPEMIEGRIDNEKVDLWCIGVLCYELLVGNPFESASHNETYRRIVKVDLKFPASVPTGAQ  
DLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV

N-glycosylation site.

60-63  
278-281

cAMP- and cGMP-dependent protein kinase phosphorylation site.

229-232

Amidation site.

192-195

Serine/Threonine protein kinases active-site signature.

196-208

Protein kinase domain

77-326

30/46

**FIGURE 27A**

GGAATTCCTTTTTTTTTTTTTTTTTGAGATGGAGTTTCACTCTTGTGGCCAGGCTGGAGTG  
CAATGGCACAATCTCAGCTTACTGCAACCTCCGCCCTCCGGGTTCAGCGATTCTCCTGC  
CTCAGCCTCTCAAGTAGCTGGGATTACAGGCATGTGCCACCACCCCTGGCTAACTAATTT  
CTTTCTATTTAGTAGAGATGGGGTTTACCCTGTTGGTCAGGCTGGTCTTGAACCTCTG  
ACCTCAGGTGATCCACTTGCCTTGGCCTCCCAAAGTGCTAGGATTACAGCCGTGAAACTG  
TGCCTGGCTGATTCTTTTTTTGTTGTTGGATTTTGAACAGGGTCTCCCTTGGTCGCCC  
AGGCTGGAGTGCAGTGGTGCATCTTGGCTCACTATAACCTCCACCTCCTGGTTTTCAAGT  
GATCCTCCCACCTTAGCCTCCTGAGTAGCTGTGATTACAGGCGTGACCACACACCCGG  
CTAATTTTTGTATTTTTATTAGAGACAGGGTTTACCCTGTTGGCCAGGCTGTTCTCAAA  
CTCCTGGACTCAAGGGATCCGCCCTGCCCTCCACTTCCCAAAGTCCCGAGATTACAGGTGTG  
AGTCACCATGCCTGACCTTATAATTTCTTAAGTCATTTTTCTGGTCCATTTCTTCCCTTAG  
GGTCCCTCACAACAAATCTGCATTAGGCGGTACAATAATCCTTAACCTTCATGATTCACAAA  
AGGAAGATGAAGTGATTCATGATTTAGAAAGGGGAAGTAGTAAGCCCACTGCACACTCCT  
GGATGATGATCCTAAATCCAGATACAGTAAAAATGGGGTATGGGAAGGTAGAATACAAAA  
TTTGGTTTAAATTAATTATCTAAATATCTAAAAACATTTTGGATACATTGTTGATGTGA  
ATGTAAGACTGTACAGACTTCTAGAAAACAGTTTGGGTTCATCTTTTTCATTTCCCCAG  
TGCAGTTTTCTGTAGAAATGGAATCCGAGGATTTAAGTGGCAGAGAATTGACAATTGATT  
CCATAATGAACAAAGTGAGAGACATTAAAAATAAGTTTAAAAATGAAGACCTTACTGATG  
AACTAAGCTTGAATAAAATTTCTGCTGATACTACAGATAACTCGGGAACGTGTTAACCAA  
TTATGATGATGGCAAACAACCCAGAGGACTGGTTGAGTTTGTGCTCAAACCTAGAGAAAA  
ACAGTGTTCGGCTAAGTGATGCTCTTTTAAATAAATTGATTGGTCGTTACAGTCAAGCAA  
TTGAAGCGCTTCCCCAGATAAATATGGCCAAAATGAGAGTTTTGCTAGAAATTCAGTGA  
GATTTGCTGAATTAAGGCTATTCAAGAGCCAGATGATGCACGTGACTACTTTCAAATGG  
CCAGAGCAAACCTGCAAGAAATTTGCTTTTGTTCATATATCTTTTGCACAATTTGAACGTG  
CACAAGGTAATGTCAAAAAAAGTAAACAACCTTCTTCAAAAAGCTGTAGAACGTGGAGCAG  
TACCACTAGAAATGCTGGAAATTTGCCCTGCGGAATTTAAACCTCCAAAAAAGCAGCTGC  
TTTCAGAGGAGGAAAAAGAAGATTTATCAGCATCTACGGTATTAACCTGCCAAGAATCAT  
TTTCCGGTTCACTTGGGCATTTACAGAATAGGAACAACAGTTGTGATTCCAGAGGACAGA  
CTACTAAAGCCAGGTTTTTATATGGAGAGAACATGCCACCACAAGATGCAGAAATAGGTT  
ACCGGAATTCATTGAGACAAACTAACAACAACTAAACAGTCATGCCCATTTGGAAGAGTCC  
CAGTTAACCTTCTAAATAGCCAGATTGTGATGTGAAGACAGATGATTCAGTTGTACCTT  
GTTTTATGAAAAGACAAACCTCTAGATCAGAATGCCGAGATTTGGTTGTGCTGGATCTA  
AACCAAGTGGAAATGATTCCTGTGAATTAAGAAATTTAAAGTCTGTTCAAAATAGTCATT  
TCAAGGAACCTCTGGTGTGATGAAAAGAGTTCTGAACCTATTATTACTGATTCAATAA  
CCCTGAAGAATAAAACGGAATCAAGTCTTCTAGCTAAATTAGAAGAACTAAAGAGTATC  
AAGAACCAGAGGTTCCAGAGAGTAACCAGAAACAGTGGCAAGCTAAGAGAAAGTCAGAGT  
GTATTAACCAGAATCCTGCTGCATCTTCAATCACTGGCAGATTCCGGAGTTAGCCCGAA  
AAGTTAATACAGAGCAGAAACATACCACCTTTTGGAGCAACCTGTCTTTTCAGTTTCAAAAC  
AGTCACCACCAATATCAACATCTAAATGGTTTGAACCAAAATCTATTTGTAAGACACCAA  
GCAGCAATACCTTGGATGATTACATGAGCTGTTTTAGAAGTCCAGTTGTAAAGAATGACT  
TTCCACCTGCTTGTGTCAGTTGTCAACACCTTATGGCCAACCTGCCTGTTTCCAGCAGCAAC  
AGCATCAATACTTGGCACTCCACTTCAAAATTTACAGGTTTACAGTCTTCTTACGCAA  
ATGAATGCATTTCCGTTAAAGGAAGATTTATTCATATTAAGCAGATAGGAAGTGGAG  
GTTCAAGCAAGGTATTTCCAGGTGTTAAATGAAAAGAAACAGATATATGCTATAAAATATG  
TGAACCTAGAAGAAGCAGATAACCAAACTCTTGATAGTTACCGGAACGAAATAGCTTATT  
TGAATAAACTACAACAACACAGTGATAAGATCATCCGACTTTATGATTATGAAATCACGG  
ACCAGTACATCTACATGGTAATGGAGTGTGGAAATATTGATCTTAATAGTTGGCTTAAAA  
AGAAAAATCCATTGATCCATGGGAACGCAAGAGTTACTGGAAAAATATGTTAGAGGCAG  
TTCACACAATCCATCAACATGGCATTGTTACAGTGATCTTAAACCAGCTAACTTTCTGA  
TAGTTGATGGAATGCTAAAGCTAATTGATTTTGGGATTGCAAACCAATGCAACCAGATA  
CAACAAGTGTGTTAAAGATTCTCAGGTGGGCACAGTTAATTATATGCCACCAGAAGCAA  
TCAAAGATATGTCTTCTCCAGAGAGAATGGGAAATCTAAGTCAAAGATAAGCCCCAAAA  
GTGATGTTTGGTCCTTAGGATGTATTTGTACTATATGACTTACGGGAAAAACACCATTTT  
AGCAGATAATTAATCAGATTTCTAAATTACATGCCATAATTGATCCTAATCATGAAATTG  
AATTTCCGATATTCCAGAGAAAGATCTTCAAGATGTGTTAAAGTGTGTTTAAAAAGGG  
ACCCAAAACAGAGGATATCCATTCTGAGCTCCTGGCTCATCCATATGTTCAAATTCAAA  
CTCATCCAGTTAACCAATGGCCAAGGGAACCACTGAAGAAATGAAATATGTTCTGGGCC  
AACTTGTGGTCTGAATTTCTCCTAACTCCATTTTGAAGCTGCTAAAACCTTATATGAAC  
ACTATAGTGGTGGTGAAAGTCATAATCTTTCATCCTCCAAGACTTTTGAAGAAAAAGGG  
GAAAAAAATGATTTGCAGTTATTCGTAATGTGATAGGAGGTATAAAATATATTGGACT  
GTTATACTCTTGAATCCCTGTGGAATCTACATTTGAAGACAACATCACTCTGAAGTGT  
ATCAGCAAAAAAATTCAGTGAGATTATCTTTAAAGAAAACGTGAAAAATAGCAACCAC

**FIGURE 27A**

TTATGGCACTGTATATATTGTAGACTTGTTTTCTCTGTTTTATGCTCTTGTGTAATCTAC  
TTGACATCATTTTACTCTTGGAATAGTGGGTGGATAGCAAGTATATTCTAAAAAAGTTTG  
TAAATAAAGTTTTGTGGCTAAATGA

32/46

**FIGURE 28**

MNKVRDIKNKFKNEDLTDELSLNKISADTTDNSGTVNQIMMMANNPEDWLSLLLKLEKNS  
 VPLSDALLNKLIGRYSQAIEALPPDKYQNESFARIQVRFAELKAIQEPDDARDYFQMAR  
 ANCKKFAFVHISFAQFELSQGNVKKSKQLLQKAVERGAVPLEMLEIALRNLNLQKKQLLS  
 EEEKNLASTVLTAQESFSGSLGHLQNRNNSCDSRGQTTKARFLYGENMPPQDAEIGYR  
 NSLRQTNKTKQSCPFGRVPVNLNLPDCDVKTDDSVVPCFMKRQTSRSECRDLVVPGSKP  
 SGNDSCELRNLSVQNSHFKEPLVSDEKSSELIITDSITLKNKTESSLLAKLEETKEYQE  
 PEVPESNQKQWQAKRKSECINQNPAASSNHWQIPELARKVNTEQKHTTTEQPVFSVSKQS  
 PPISTSKWFDPKSICKTPSSNTLDDYMSCFRTPVVKNDFFPACQLSTPYGQPACFQQQQH  
 QILATPLQNLQVLASSSANECISVKGRIYSILKQIGSGGSSKVFQVLNEKKQIYAIKYVN  
 LEEADNQTLDYSRNEIAYLNKLQQHSDDKIIRLYDYEITDQYIYMMECGNIDLNSWLKKK  
 KSIDPWERKSYWKNMLEAVHTIHQHGIVHSDLKPANFLIVDGMLKLIDFGIANQMOPDTT  
 SVVKDSQVGTNVNMPPEAIKDMSSSRENGKSKSKISPKSDVWSLGCILYYMTYGKTPFQQ  
 IINQISKLHAIIDPNHEIEFPDIPEKDLQDVLKCLKRDPKQRISIPELLAHPYVQIQTH  
 PVNQMAKGTTEEMKYVLGQLVGLNSPNSILKAAKTLYEHYSGGESHNSSSSKTFEKKRGK  
 K

N-glycosylation site.

90-93  
 186-189  
 210-213  
 247-250  
 303-306  
 342-345  
 546-549  
 827-830

cAMP- and cGMP-dependent protein kinase phosphorylation site.

282-285  
 374-377  
 599-602

Tyrosine kinase phosphorylation site.

351-358  
 787-796

N-myristoylation site.

88-93  
 297-302  
 302-307  
 470-475  
 516-521  
 626-631  
 798-803

Amidation site.

838-841

Serine/Threonine protein kinases active-site signature.

627-639

Protein kinase domain

509-775



**FIGURE 29**

GAATTCGCGGCCGCGCTCGACGATCTCTTGGAGACGGCGACCCAGGCATCTGGGGAGCCAC  
AGAAGTCGTACTCCCTTAAACCCTGCTTTGCTCCCCCTGTGGATGTAACCCCTTAGCTGG  
CATTTTGCATCTCAATTGGCTTGTGATGGAGGCGTCTTTGGGGATTGAGATGGATGAGCC  
AATGGCTTTTTCTCCCCAGCGTGACCGGTTTCAGGCTGAAGGCTCTTTAAAAAAAACGA  
GCAGAATTTTAACTTGCAGGTGTTAAAAAAGATATTGAGAAGCTTTATGAAGCTGTACC  
ACAGCTTAGTAATGTGTTTAAAGATTGAGGACAAAATTGGAGAAGGCACTTTCAGCTCTGT  
TTATTTGGCCACAGCACAGTTACAAGTAGGACCTGAAGAGAAAATTGCTCTAAACACTT  
GATTTCCAACAAGTCATCCTATAAGAATTGCAGCTGAACCTTCAGTGCCTAACAGTGGCTGG  
GGGGCAAGATAATGTCATGGGAGTTAAATACTGCTTTAGGAAGAATGATCATGTAGTTAT  
TGCTATGCCATATCTGGAGCATGAGTCGTTTTTGGACATTCTGAATTCTCTTTCCTTTCA  
AGAAGTACGGGAATATATGCTTAATCTGTTCAAAGCTTTGAAACGCATTTCATCAGTTTGG  
TATTGTTTACCCTGATGTTAAGCCCAGCAATTTTTTATATAATAGGCGCCTGAAAAAGTA  
TGCTTTGGTAGACTTTGGTTTGGCCCAAGGAACCCATGATACGAAAATAGAGCTTCTTAA  
ATTTGTCCAGTCTGAAGCTCAGCAGGAAAGGTGTTCAAAAACAAATCCACATAATCAC  
AGGAAACAAGATTCCACTGAGTGGCCAGTACCTAAGGAGCTGGATCAGCAGTCCACCAC  
AAAAGCTTCTGTTAAAAGACCTACACAAATGCACAAATTCAGATTAAACAAGGAAAAGA  
CGGAAAGGAGGGATCTGTAGGCCCTTCTGTCCAGCGCTCTGTTTTTGGAGAAAGAAATTT  
CAATATACACAGCTCCATTTTACATGAGAGCCCTGCAGTGAACCTCATGAAGCAGTCAAA  
GACTGTGGATGTACTGTCTAGAAAGTTAGCAACAAAAAGAAGGCTATTTCTACGAAAGT  
TATGAATAGTGTCTGTGATGAGGAAACTGCCAGTTCTTGGCCAGCTAGCCTGACCTGTGA  
CTGCTATGCAACAGATAAAGTTTGTAGTATTTGCCTTTCAAGGCGTCAGCAGGTTGCCCC  
TAGGGCAGGTACACCAGGATTCAGAGCACCAGAGGTCTTGACAAAGTGCCCCAATCAAAC  
TACAGCAATTGACATGTGGTCTGCAGGTGTCAATATTTCTTTGCTTAGTGGACGATA  
TCCATTTTATAAAGCAAGTGATGATTTAACTGCTTTGGCCCAAATTATGACAATTAGGGG  
ATCCAGAGAAACTATCCAAGCTGCTAAACCTTTTGGGAAATCAATATTATGTAGCAAAGA  
AGTTCACAGCACAAAGCTTGAGAAAACCTCTGTGAGAGACTCAGGGGTATGGATTCTAGCAC  
TCCCAAGTTAAACAAGTGATATACAAGGGCATGCTTCTCATCAACCAGCTATTTTCAGAGAA  
GACTGACCATAAAGCTTCTGCTCGTTCAAACACCTCCAGGACAATACTCAGGGAATTC  
ATTTAAAAAGGGGGATAGTAATAGCTGTGAGCATTGTTTTGATGAGTATAATACCAATTT  
AGAAGGCTGGAATGAGGTACCTGATGAAGCTTATGACCTGCTTGATAAACTTCTAGATCT  
AAATCCAGCTTCAAGAATAACAGCAGAAGAAGCTTTGTTGCATCCATTTTTTAAAGATAT  
GAGCTGTGATAATGGATCTTCATTTAATGTTTACTGTTATGAGGTAGAATAAAAAAGAA  
TACTTTGTAAAGACCAAGTTCTTGTTTAGAGACCAGAGCAGGATTAATAATTTATTTT  
AACATTTTAGTGTGTTGGTGGCACATTCTAAAATATAGATTAAAGAACTTAAAAATGCCTG  
GGATAGTTCTTGGGACTAACACATGATCTTCTTTGAGTTAAACCTACCTAAGTAGATTT  
TAGGTGGGTTCCTATTAGGTCAGATTTTGTAGCTTCCCTAATTACCTTTCACTGACATACA  
GAAAAAGGAGCAGTTTTAGTTTTAATTAATTAATAAATAACAGATGTGATGAGGATTAAAT  
GAATCAAAAAGACTTAATTTGTAGATTCTTTTAGAGTTATGAGCTAGGTATAGTTTGGGGA  
AACTCAACCTGGTGTGCTGCTTAAACAATTTGTAAATAAAGAAGATAATTTCTCTTTT  
CTAGAGGTACATATTAGGCCTTTTATGAACACTAAAACAATGAGGAAATGTTGGTCATGG  
GGCAAAGTATCACTTAAATTTGAATTCATCCATTTTTAAAAAACACTTCATGAAAGCATT  
CTGGTGTGAATTGCCATTTTTTCTTACTGGCTTCTCAATTTTCTTCTCTGCCCCCT  
ACCTAAAACATTCTCCTCGGAAATTACATGGTGCTGACCACAAAGTTTCTGGATGTTTTA  
TTAAATATTGTACGTGTTTACAGTTGGGAATTTAAATAATACATACACTGGTTGATAAA  
GGGAAGCTGCAGGACCAAGGTGAAGATTGATAGTCCAAATGCTTTTCTTTTTTGTAGTTGT  
ATATTTTTTTCACACCATCTTAGATATAATTAGGTAGCTGCTGAAAGGAAAAGTGAATACA  
GAATTGACGGTATTATTGGAGATTTTTCTCTGCGTAGAGCCATCCAGATCTCTGTATCC  
TGTTTTGACTAAGTCTTAGGTGGGTGGGAAGACAGATAATGAAGTAGGCAAAGAGAAAA  
GGACCAAGATAGAGGTTTATATTAGAAATGGTATATATCAATGACAGCATATCAAACCT  
TCCTATGGGAAAAAGTCTGGTGGGTGGTCAGCTGACAGATTTCCCATTTAGTAGTCATAG  
AATACAGAAATAGTTTAGGGACATGTATTCATTTTGTATTTTGTAGCATTGATAGGTCAG  
TATATCTACCTAATCTGTTTGGTAAAGTATAGGATATATAAACCATTACCATTGATCTGTC  
TTATGCCATAATCTTAAAAAAAATGAATGCTCTTGAATTTGTATATTCAATAAAGTTA  
TCCTTTTATAAAAAAAAAGTCGACGCGGCCGC

34/46

**FIGURE 30**

MEASLGIQMDEPMAFSPQRDRFOAEGSLKKNEQNFKLAGVKKDIEKLYEAVPQLSNVFKI  
EDKIGEGTFSSVYLATAQLQVGPEEKIALKHLIPTSHPIRIAAELQCLTVAGGQDNVMGV  
KYCFRKNHDHVVIAMPYLEHESFLDILNSLSFQEVREYMLNLFKALKRIHQFGIVHRDVKP  
SNFLYNRRLKKYALVDFGLAQGTHDTKIELLKFFVQSEAQQERCSONKSHIITGNKIPLSG  
PVPKELDQQSTTKASVKRPYTNAQIQIKQKGKDGKEGSLVQSVFGERNFNIHSSISH  
ESPAVKLMKQSKTVDVLSRKLATKKKAISTKVMNSAVMRKTASSCPASLTCDYATDKVC  
SICLSRRQOVAPRAGTPGFRAPEVLTKCPNQTTAIDMWSAGVIFLSLLSGRYPFYKASDD  
LTALAQIMTIRGSRETIQAAKTFGKSILCSKEVPAQDLRKLCELRGMDSSTPKLTSDIQ  
GHASHQPAISEKTDHKASCLVQTPPGQYSGNSFKKGDSNSCEHCFDEYNTNLEGWNEVPD  
EAYDLLDKLLDLNPASRITAEALLHPFFKDMSL

N-glycosylation site.

226-229  
390-393

Tyrosine kinase phosphorylation site.

41-48

N-myristoylation site.

67-72  
112-117  
119-124  
198-203  
202-207  
432-437  
467-472  
506-511

ATP/GTP-binding site motif A (P-loop).

439-446

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain

58-569

35/46

**FIGURE 31**

CCGAGTTACGAGTCGGCGAAAGCGGGCGGGAAGTTCGTACTGGGCAGAACGCGACGGGTCT  
GCGGCTTAGGTGAAAATGCCTCGTGTAAGCAGCTCAAGCTGGAAGACAGAGCTCTGCA  
AAGAGACATCTTGCAGAACAATTTGCAGTTGGAGAGATAATAACTGACATGGCAAAAAAG  
GAATGGAAAGTAGGATTACCCATTGGCCAAGGAGGCTTTGGCTGTATATATCTTGCTGAT  
ATGAATTCCTCAGAGTCAGTTGGCAGTGATGCACCTTGTGTTGTAAAAGTGGAAACCCAGT  
GACAATGGACCTCTTTTTACTGAATTAAAGTTCTACCAACGAGCTGCAAAACCAGAGCAA  
ATTCAGAAATGGATTTCGTACCCGTAAGCTGAAGTACCTGGGTGTTCCCTAAGTATTGGGGG  
TCTGGTCTACATGACAAAAATGGAAAAAGTTACAGGTTTATGATAATGGATCGCTTTGGG  
AGTGACCTTCAGAAAATATATGAAGCAAATGCCAAAAGGTTTTCTCGGAAAACGTCTTG  
CAGCTAAGCTTAAGAATTCTGGATATTCTGGAATATATTCACGAGCATGAGTATGTGCAT  
GGAGATATCAAGGCCCTCAAATCTTCTTCTGAAC TACAAGAATCCTGACCAGGTGTACTTG  
GTAGATTATGGCCTTGCTTATCGGTACTGCCCAGAAGGAGTTCATAAAGAATACAAAGAA  
GACCCCAAAGATGTCACGATGGCACTATTGAATTCACGAGCATCGATGCACACAATGGT  
GTGGCCCCATCAAGACGTGGTGATTTGGAAATACCTTGTTTATTGCATGATCCAATGGCTT  
ACTGGCCATCTTCCTTGGGAGGATAATTTGAAAGATCCTAAATATGTTAGAGATTCCAAA  
ATTAGATACAGAGAAAATATTGCAAGTTTGATGGACAAATGTTTCTCTGAGAAAAACAAA  
CCAGGTGAAATTGCCAAATACATGGAAACAGTGAAATTACTAGACTACACTGAAAAACCT  
CTTTATGAAAATTTACGTGACATTCTTTTGCAAGGACTAAAAGCTATAGGAAGTAAGGAT  
GATGGCAAATTTGGACCTCAGTGTTGTGGAGAATGGAGGTTTGAAAGCAAAAAACAATAACA  
AAGAAGCGAAAGAAAGAAATTGAAGAAAGCAAGGAACCTGGTGTTGAAGATACGGAATGG  
TCAAACACACAGACAGAGGAGGCCATACAGACCCGTTCAAGAACCAGAAAGAGAGTCCAG  
AAGTAATTCAGATGCTGTGAACCAGATTTCTTTTCTTTGTTTTCTTTTGACTTTTTTCT  
CCTTTTCTGTGTTAGAACTGTTTTATTTTCTGTGAGTCTTGCGAGGTGGAATTAATGATTA  
AATACTCATGTGTTTCAAGAAACATAAACTTTTTTTATAAAAAATATTTTGTACAATTCATT  
AAAGGCTAATTTATGAAATTTGAAATCTTCAGGTTATACTCCTTAAGTTATCCCAAAGC  
CGTGTGTTTGTGATGTTTTGGAGTACATATATATGAAAATTATTATGACACGCACTTTTC  
TAATCATTGTACATTTCTCAGAGTGGATAAAAAATGTTTGACAAAGTCCTCACTTTTAAGG  
AAATGCAAAGCTTAAAAATAAACTCTTTTTGTTTGTATGCAG

36/46

**FIGURE 32**

MPRVKAAQAGRQSSAKRHAEQFAVGEIITDMAKKEWKVGLPIGQGGFGCIYLADMNSSE  
SVGSDAPCVVKVEPSDNGPLFTELKFYQRAAKPEQIQKWIRTRKLKYLGVPKYWGSGLHD  
KNGKSYRFMIMDRFGSDLQKIYEANAKRFSRKTVLQLSLRILDILEYIHEHEYVHGDIKA  
SNLLLNKPNPDQVYLVLDYGLAYRYCPEGVHKEYKEDPKRCHDGTIEFTSIDAHNGVAPSR  
RGDLEILGYCMIQWLTGHLPWEDNLKDPKYVRDSKIRYRENIASLMDKCFPEKNKPGEIA  
KYMETVKLLDYTEKPLYENLRDILLQGLKAIGSKDDGKLDLSVVENGGLKAKTITKKRKK  
EIEESKEPGVEDTEWSNTQTEEAIQTRSRTRKRVQK

N-glycosylation site.

57-60

cAMP- and cGMP-dependent protein kinase phosphorylation site.

147-150

Tyrosine kinase phosphorylation site.

160-167

188-194

241-249

295-302

N-myristoylation site.

40-45

46-51

235-240

347-352

369-374

Cell attachment sequence.

241-243

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain

37-325

**FIGURE 33**

AGTTGGCGGGAATGGCTGCTCGCGGAGGGGCGAGTGTACGCGGGGCCGCTGTAGGCTGTCC  
AGCGATGGATCCACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGA  
GGGCGTGAATAGGATCGCAGTGCCAAAGCCGCCCTCCATTGAGGAATTCAGCATAGTGAA  
GCCCATTAGCCGGGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTA  
TGCAGTAAAGGTTGTTAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCA  
AGCTGAGAGAGATGCACTGGCACTAAGCAAAAGCCCATTTCATTGTCCATTTGTATTATTC  
ACTGCAGTCTGCAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAA  
GTCTCTCCTACATATATATGGTTATTTTGTATGAAGAGATGGCTGTGAAATATATTTCTGA  
AGTAGCACTGGCTCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACC  
GGACAATATGCTTATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAA  
AGTTACTTTGAATAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAA  
ACCTAGACAAGATTATTCAAGAACCCAGGACAAGTGTTATCGCTTATCAGCTCGTTGGG  
ATTTAACACACCAATTGCAGAAAAAATCAAGACCCTGCAACATCCTTTAGCCTGTCT  
GTCTGAAACATCACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGA  
CACTACGCCTTATTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCC  
AGGAATGCCTGTGAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCAC  
ATCCAGTGCCAGTAGTCAATCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAG  
CAGTCCCAAATGGGAAAAAGATTGCCAGGAAAGTGATGAAGCATTGGGCCCCAACAATGAT  
GAGTTGGAATGCAGTTGAAAAGTTATGCGCAAAATCTGCAATGCCATTGAGACGAAAGG  
TTTCAATAAAAAGGATCTGGAGTTAGCTCTTTCTCCATTTCATAACAGCAGTGCCTTCC  
CACCCTGGACGCTCTTGTGTAAACCTTGCTAAAAAATGCTTCTCTGGGGAAGTTTCTTG  
GGAAGCAGTAGAAGTGGATGTAAATAATATAAATATGGACACTGACACAAGTCAGTTAGG  
TTTCCATCAGTCAAATCAGTGGGCTGTGGATTCTGGTGGGATATCTGAAGAGCACCTTGG  
TTGAAAGAAGTTAAAAAGAAATTTTGAAGTTGGTTGACTCCAGTCTTGTAAAAAATTA  
ACAGAATAAAAAAATCTGTGTAGAGTATAAGCATAACGAAATGACAAATTTGTATACAAA  
TCAAAATACAGGCTTAACAGTTGAAGTGCAGGACCTTAAGCTATCAGTGCACAAAAGTCA  
ACAAAATGACTGTGCTAATAAGGAGAACATTGTCAATTCCTTTACTGATAAACAACAAC  
ACCAGAAAAATTACCTATACCAATGATAGCAAAAAACCTTATGTGTGAAGTGCATGAAGA  
CTGTGAAAAGAAATAGTAAGAGGGACTACTTAAGTTCTAGTTTCTATGTTCTGATGATGA  
TAGAGCTTCTAAAAATATTTCTATGAAGTCTGATTCTCTTTCTGGAATTTCTATAAT  
GGAAAGTCCATTAGAAAAGTCAGCCCTTAGATTTCAGATAGAAGCATTAAAGAATCCTCTTT  
TGAAGAATCAAATATGAAGATCCACTTATTGTAAACACCAGATTGCCAAGAAAAGACCTC  
ACCAAAGGTGTCGAGAACCTTGCTGTACAAGAGAGTAACCAAAAAATGTTAGGTCTCTC  
TTTGGAGGTGCTGAAAACGTTAGCCTCTAAAAGAAATGCTGTTGCTTTTCGAAGTTTAA  
CAGTCATATTAATGCATCCAATAACTCAGAACCATCCAGAATGAACATGACTTCTTTAGA  
TGCAATGGATATTTTCGCGTGCCTACAGTGGTTCATATCCCATGGCTATAACCCCTACTCA  
AAAAAGAGATCCTGTATGCCACATCAGACCCCAATCAGATCAAGTCGGGAAGTCCATA  
CCGAAGTCCGAAGAGTGTGAGAAGAGGGGTGGCCCCCGTTGATGATGGGCGAATTCTAGG  
AACCCAGACTACCTTGACCTGAGCTGTTACTAGGCAGGGCCCATGGTCTCTGCGGTAGA  
CTGGTGGGCACTTGGAGTTTGCTTGTGTTGAATTTCTAACAGGAATTTCCCCCTTCAATGA  
TGAAACACCACAACAAGTATTCCAGAATATCTGAAAAGAGATATCCCTTGCCAGAAAGG  
TGAAGAAAAGTTATCTGATAATGCTCAAAGTGCAGTAGAAATACTTTTAACCATTGATGA  
TACAAAGAGAGCTGGAATGAAAGAGCTAAAACGTCATCTCTCTTCAGTGATGTGGACTG  
GGAAAATCTGCAGCATCAGACTATGCCTTTCATCCCCCAGCCAGATGATGAAACAGATAC  
CTCCTATTTTGAACACAGGAATACTGCTCAGCACCTGACCGTATCTGGATTTAGTCTGTA  
GCACAAAAATTTTCTTTTAGTCTAGCCTCGTGTTATAGAATGAAGTGCATAATTATAT  
ACTCCTTAATACTAGATTGATCTAAGGGGGAAAGATCATTATTTAACCTAGTTCAATGTG  
CTTTTAATGTACGTTACAGCTTTACAGAGTTAAAAGGCTGAAAGGAATATAGTCAGTAA  
TTTATCTTAACCTCAAACTGTATATAAATCTTCAAAGCTTTTTCATCTATTTATTTTG  
TTTATTGCACTTTATGAAAAGTGAAGCATCAATAAAATAGAGGACACTATTGAGAGTGA  
GCCACTAGCTTGATTTTCTTTCTCTCTGATTTTCAGTTCACTGTTTCAGTTTAGCATTA  
ATAATAAAATAATCATACAGTTCC

38/46

**FIGURE 34**

MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLGQKGGKLYA  
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGGDVKS  
LLHIYGYFDEEMAVKYI SEVALALDYLHRHGIIHRDLKPDNMLISNEGH IKLTD FGLSKV  
TLNRDINMMDILTTSPMAKPRQDYSRTPGQVLSLISSLG FNTPIAEKNQDPANILSACLS  
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS  
SASSQSHTFISSVESECHSSPKWEKDCQESDEALGPTMMSWNAVEKLC AKSANAIETKGF  
NKKDLELALSPIHNSSALPTTGRSCVNLAKKCFSGEVSWEAVELDVNNINMDTDTSQLGF  
HQSNQWAVDSGGISEEHLGKRSLKRN FELVDSSPCKKIIQNKKTCVEYKHNEMTNCYTNO  
NTGLTVEVQDLKLSVHKSQQNDCANKENIVNSFTDKQQTPEKLPIPMIAKNLMCELEDC  
EKNSKRDYLSSSF L C S D D D R A S K N I S M N S D S S F P G I S I M E S P L E S Q P L D S D R S I K E S S F E  
ESNIEDPLIVTPDCQEKTS PKGVENPAVQESNQMLGPPLEVLKTLASKRNAVAFRSFNS  
HINASNNSEPSRMNMTSLDAMDISRAYS GSY PMAITPTQKRRSCMPHQTPNQIKSGTPYR  
TPKSVRRGVAPVDDGRILGTPDYLAPELLLGRAHGPAVDWWALGVCLFEFLTGI PPFNDE  
TPQQVFQNILKRDI PWPEGEEKLSDNAQSAVEILLTIDDTKRAGMKELKRHPLFSDVDWE  
NLQHQTMPFIPQPDDETDTSYFETRNTAQHLTVSGFSL

N-glycosylation site.

73-76  
374-377  
564-567  
663-666  
666-669  
674 -677

CAMP- and cGMP-dependent protein kinase phosphorylation site.

700-703

N-myristoylation site.

12-17  
13-18  
52-57  
209-214

Amidation site.

438-441

Serine/Threonine protein kinases active-site signature.

152-164

Protein kinase domain

35-834

39/46

**FIGURE 35**

CAAGAGCCCTTCCTGCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAA  
CCACTTACAGGCCGGAAGTGTCGGGGTGGACGCATTCTGGGTAGCCGAAGAAGTCCCAGG  
ATTGCCGAAGAAGTCCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTCAGAG  
ACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACG  
CCGGCCGATGGCGAGGAGCCCCCGGGAGGCTGAGGCTCTGGCCGCGAGCCCGGGAACGG  
AGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCTGTTT  
CGTGGCCGCTTCCAGGGCCGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGG  
CACCCGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGACAGGAGGCCCGGGCGCTC  
CTCCGCTGTCGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCC  
AACTGCTTATATATGGAAGAAATTGAAGGCTCAGTGAAGTTCGAGATTATATTCAGTCC  
ACTATGGAGACTGAAAAAACTCCCCAGGGTCTCTCCAAGTACCAAGACAATTGGGCAG  
GTTTTGGCTCGAATGCACGATGAAGACCTCATTGATGTTGATCTCACCACCTCCAACATG  
CTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTC  
ATTTACAGCACTTCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCCTC  
AGTACCCATCCCAACACTGAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCC  
TCCAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAG  
AGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACACACACAGTGAAGCTCTTTTTTC  
AAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGAT  
ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

40/46

**FIGURE 36**

MAAARATTPADGEEPAPEAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK  
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFVVDYASNCLYMEEIEGSV  
TVRDYIQSTMETEKTPOGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV  
LIDFGLSFISALPEDKGVLDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD  
EVRLRGRKRSMVG

cAMP- and cGMP-dependent protein kinase phosphorylation site.

78-81  
247-250

N-myristoylation site.

147-152

Amidation site.

76-79  
245-248

Tyrosine protein kinases specific active-site signature.

158-170

Protein kinase domain

33-252



41/46

**FIGURE 37**

AGCGCGCGACTTTTTGAAAGCCAGGAGGGTTCGAATTGCAACGGCAGCTGCCGGGCGTAT  
GTGTTGGTGCTAGAGGCAGCTGCAGGGTCTCGCTGGGGGCCGCTCGGGACCAATTTTGAA  
GAGGTACTTGGCCACGACTTATTTTCACCTCCGACCTTTCCTTCCAGGCGGTGAGACTCT  
GGACTGAGAGTGGCTTTTCACAATGGAAGGGATCAGTAATTTCAAGACACCAAGCAAATTA  
TCAGAAAAAAGAAATCTGTATTATGTTCAACTCCAACATAAAATATCCCGGCCTCTCCG  
TTTATGCAGAAAGCTTGGCTTTGGTACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCA  
AGAGGTTTGTCTCATTCTCCTTGGGCTGTAAAAAAGATTAATCCTATATGTAATGATCAT  
TATCGAAGTGTGTATCAAAAGAGACTAATGGATGAAGCTAAGATTTTGAAAAGCCTTCAT  
CATCCAAAACATTGTTGGTTATCGTGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTCTT  
GCTATGGAATATGGAGGTGAAAAGTCTCTAAATGACTTAATAGAAGAACGATATAAAGCC  
AGCCAAGATCCTTTTCCAGCAGCCATAATTTTAAAGTTGCTTTGAATATGGCAAGAGGG  
TTAAAGTATCTGCACCAAGAAAAGAACTGCTTCATGGAGACATAAAGTCTTCAAATGTT  
GTAATTAAGGCGATTTTGAACAAATTAATAATCTGTGATGTAGGAGTCTCTTACCCTG  
GATGAAAATATGACTGTGACTGACCCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAA  
CCCAAAGAAGCTGTGGAGGAGAATGGTGTATTACTGACAAGGCAGACATATTTGCCTTT  
GGCCTTACTTTGTGGGAAATGATGACTTTATCGATTCCACACATTAATCTTTCAAATGAT  
GATGATGAAGATAAACTTTTGATGAAAGTGATTTTGATGATGAAGCATACTATGCA  
GCGTTGGGAAGTAGGCCACCTATTAATATGGAAGAAGTGGATGAATCATACCAGAAAGTA  
ATTGAACTCTTCTGTATGCACTAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACAC  
ATTGTTGAAGCTCTGGAACAGATGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCGT  
AAATAACTGTTTATTCCAAAATATTTACATAGTTACTATCAGTAGTTATTAGACTCTAAA  
ATTGGCATATTTGAGGACCATAGTTTCTTGTTAACATATGGATAACTATTTCTAATATGA  
AATATGCTTATATTGGCTATAAGCACTTGGAAATGTACTGGGTTTTCTGTAAAGTTTTAG  
AACTAGCTACATAAGTACTTTGATACTGCTCATGCTGACTTAAACACTAGCAGTAAAA  
CGCTGTAAACTGTAAACATTAAATTGAATGACCATTACTTTTATTAATGATCTTTCTTAAA  
TATTCTATATTTAATGGATCTACTGACATTAGCACTTTGTACAGTACAAAATAAAGTCT  
ACATTTGTTTTAAACACTGAACCTTTTGTGATGTGTTTATCAAATGATAACTGGAAGCT  
GAGGAGAATATGCCTCAAAAAGAGTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATT  
GTCTTGATCTCTTGGATCTCCTCAGATCTTTGGTTTTTGCTTTAATTTATTAAATGTATT  
TTCCATACTGAGTTTAAATTTTATTAATTTGTACCTTAAGCATTTCCAGCTGTGTAAAA  
ACAATAAACTCAAATAGGATGATAAAGAATAAAGGACACTTTGGGTACCAGAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

42/46

**FIGURE 38**

MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTG VNVYLMKRSPRGLSHSP  
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGGE  
KSLNDLIEERYKASQDPFPAAILKVALNMARGGLKYLHQEKLLHGDIKSSNVVIKGDFF  
TIKICDVGVSPLDENMTVTDPEACYIGTEPWKPKEAVEENGVITDKADIFAFGLTLWEM  
MTLSIPHINLSNDDDDDEKTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIELFSVC  
TNEDPKDRPSAAHIVEALETDV

N-glycosylation site.

196-199

249-252

cAMP- and cGMP-dependent protein kinase phosphorylation site.

16-19

N-myristoylation site.

41-46

118-123

Serine/Threonine protein kinases active-site signature.

163-175

Protein kinase domain

32-320

**FIGURE 39**

GTGCGATCCCGGGCCCGAGGGCATCAGACGGCGGCTGATTAGCTCCGGTTTGCATCACCC  
GGACCGGGGGATTAGCTCCGGTTTGCATCACCCGGACCGGGGGCCGGGCGCGCACGAGAC  
TCGCAGCGGAAGTGGAGGCGGCTCCGCGCGCGTCCGCTGCTAGGACCGGGCAGGGCTGG  
AGCTGGGCTGGGATCCCGAGCTCGGCAGCAGCGCAGCGGGCCGGCCACCTGCTGGTGCC  
CTGGAGGCTCTGAGCCCCGGCGGCGCCCGGGCCACGCGGAACGACGGGGCGAGATCGGA  
GCCACCCCTCTAGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGAT  
GACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGA  
CTGCCCCCTGCCTGTTGCCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTG  
GCCACTGCCCTCCCGTCTTGGGCCCTATGTCTCCTGGAGCCCCGAGGAGGGCGGGCGGGCC  
TACCAGGECCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAG  
GAAGCCCCGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCCGCACAAAGCATGTGGCTCGG  
CCCACTGAGGTCTGGCTGGTACCCAGCTCCTCTACGCCTTTTTCTACTCGGACCCATGGG  
GACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTC  
TTCCGCCAGATGGCCACCGCCCTGGCGCACTGTACACAGCACGGTCTGGTCTGCGTGAT  
CTCAAGCTGTGTGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTGGAGAAC  
CTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGC  
CCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCC  
GATGTCTGGAGCCTGGGCGTGGCGCTCTTACCATGCTGGCCGGCCACTACCCCTTCCAG  
GACTCGGAGCCTGTCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCTGCA  
GGCCTCTCGGCCCTGCCCGCTGTCTGGTTGCTGCTCCTTCGTGGGAGCCAGCTGAA  
CGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCTTA  
GCCCCAACCCGATCCCATCTCTGGGAGGCTGCCAGGTGGTCCCTGATGGTCTGGGGCTG  
GACGAAGCCAGGGAAGAGGAGGGAGACAGAGAAGTGGTTCTGTATGGCTAGGACCACCCT  
ACTACACGCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGTAGCTCCAAGCCTTCTCCTG  
CCTCTGAAGTGAAGCAACCTTCACTGCCTTCCAGAAGGGAGAAAGGCAGAAGCCTGTGT  
GGAGTGTGCTGTGTACACATCTGCTTTGTTCCACACACATGCAGTTCTCTGCTTGGGTGCT  
TATCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAAT  
ATTCCTGCTCACAGAGATGACAACTGGCATCCTTGAGCTGACAACACTTTTCCATGAC  
CATAGGTCACTGTCTACACTGGGTACACTTTGTACCAAGTGTGCGCCTCCACTGATGCTGG  
TGCTCAGGCACCTCTGTCCAAGGACAATCCCTTTCACAAACAAACCAGCTGCCTTTGTAT  
CTTGTTACCTTTTTCAGAGAAAGGGAGGTATCCCTGTGCCAAGGCTCCAGGCCTCTCCCT  
GCAACTCAGGACCCAAGCCAGCTCACTCTGGGAAGTGTGTTCCCAGCATCTCTGTCTC  
TTGATTAAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCC  
AAACTATGAGGCTAGTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTG  
TCAACCATGGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTG  
TCCTGTGGCCACCTGGAAAGTCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAA  
TCCAGGTCCATACTCTAGGTTTTGGATACCATGAGTATGTATGTTTACCTGTGCCTAAT  
AAAGGAGAATTATGAAATAAAAAAAAAAAAAAAAAA

44/46

**FIGURE 40**

MRATPLAAPAGSLSRKKRLEDDNLDTERPVQKRARSGPQPRLPCLLPSPPTAPDRAT  
AVATASRLGPYVLLPEEGGRAYQALHCPTGTEYTCKVYPVQEAPAVLEPYARLPPhKHV  
ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL  
RDLKLCRFVFADRERKKLVLENLEDSVLTGPDDSLWDKHACPAYVGPEILSSRASYSK  
AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP  
AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLG

N-myristoylation site.

91-96  
341-346

Protein kinase domain

71-315

45/46

**FIGURE 41**

GAAGTTTCTCACTAGGGTCTTCTCTGGCCCAGCCTTTGACTGAAGCTGGTCTGGAGACAG  
GGGCATTAGAGAAGTGACTCATAGATGGCCTAAAGAAGCGGGGCCACTCAAGGACCCAGG  
ACAGAGGGAAGAGGGCCAACCCAGCTGGACCACAGGCAAACCCATTGCCCTTTGAGAGAA  
AGAAGAGGACCCGGTGAACATGCTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCG  
TCTACGAGATCCGCGAGAGGCTCGGCTCGGGTGCCTTCTCCGAGGTGGTGTGGCCCAGG  
AGCGGGGCTCCGCACACCTCGTGGCCCTCAAGTGCATCCCCAAGAAGGCCCTCCGGGGCA  
AGGAGGCCCTGGTGGAGAACGAGATCGCAGTGCTCCGTAGGATCAGTCACCCCAACATCG  
TCGCTCTGGAGGATGTCCACGAGAGCCCTTCCCACCTCTACCTGGCCATGGAAGTGGTGA  
CGGGTGGCGAGCTGTTTGACCGCATCATGGAGCGCGGCTCCTACACAGAGAAGGATGCCA  
GCCATCTGGTGGGTGAGTCCCTTGGCGCCGTCTCCTACCTGCACAGCCTGGGGATCGTGC  
ACCGGGACCTCAAGCCCGAAAACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCA  
TGGTCTCTGACTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTG  
GGACCCCTGGATATGTGGCCCCAGAGCTCTTGGAGCAGAAACCTACGGGAAGGCCGTAG  
ATGTGTGGGCCCCGGGCGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTACG  
ACGAGAGCGACCCTGAGCTCTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTXTC  
CTTTCTGGGATGACATCTCAGAATCAGGCAAAGACTTTATTTCGGCACCTTCTGGAGCGAG  
ACCTTCAGAAGAGGTTACCTGCCAACAGGCCCTTGCGGGACCTTTGGATCTTTTGGGACA  
CAGGCTTTGGCAGGGACATCTTAGGGTTTGTCAGTGAGCAGATCCGGAAGAACTTTGCTT  
GGACACACTGGAAGCGAGCCTTCAATGCCACCTTGTTTCCTGCGCCACATCCGGAAGCTGG  
GGCAGATCCCAGAGGGCGAGGGGGCCTCTGAGCAGGGCATGGSCCGXCACAGCCACTXAG  
GCCTTCGTGCTGGCCAGCCCCCAAGTGGATGCCCAGGXAGATGCCGAGGCCAAGTGG  
AXTGAXCCCCAGATTTXCTTXC

46/46

**FIGURE 42**

MLLLKKHTEDISSVYEIRERLGSGAFSEVVLAQERGS AHLVALKCIPKKALRGKEALVEN  
EIAVLRRI SHPNIVALEDVHESPSHLYLAMELV TGGELFDRIMERGSYTEKDASHLVGQV  
LGAVSYLHSLGIVHRDLKPENLLYATPFEDSKIMVSD FGLSKIQAGNMLGTACGTPGYVA  
PELLEQKPYGKAVDVWALGVISYILLCGYPPFFYDES DPELFSQILRASYEFDXPFWD DIS  
ESGKDFIRHLLERDLQKRFTCQQALRDLWIFWDTGFGRDILGFVSEQIRKNFAWTHWKRA  
FNATLFLRHIRKLGQIPEGEGASEQGMXRHSHXGLRAGQPPKW

N-glycosylation site.

302-305

cAMP- and cGMP-dependent protein kinase phosphorylation site.

5-8

66-69

257-260

Tyrosine kinase phosphorylation site.

101-108

N-myristoylation site.

118-123

166-171

170-175

334-339

Serine/Threonine protein kinases active-site signature.

132-144

Protein kinase domain

15-270